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Length 15;
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Fatent No. 6084063
GENERAL INFORMATION:
APPLICANT: Vonakis, Becky
APPLICANT: Chen, Hearian
TITLE OF INVENTION: SIGNAL TRANSDUCTION INHIBITORS
TITLE OF INVENTION: OF ALLERGIC REACTIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: NEEDLE & ROSENBERG, P.C.
: SUITE 1200, 127 PEACHTREE STREET
ATLANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.9%; Score 7; DB 5
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: CCOR-0232
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14014.0285
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-9880
TELEFAX: 404/688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MILLER, MARY L
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide PCT-US95-04018-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 QPTPEPS 358
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 30303
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Sequence 59 Application PC/TUS9504018
Sequence 59 Application PC/TUS9504018
Sequence 59 Application PC/TUS9504018
Sequence 59 Application PC/TUS9504018
Sensity Cant. Horomation Carrier APPLICANT: Mervic, Marian APPLICANT: Mervic, Miljenko APPLICANT: Mober Nober Washburn Kurtz Mackiewicz & ADDRESSEE: Nooris ADDRESSEE: Nooris STREET: One Liberty Place 46th Floor CITY: Philadelphia STREET: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
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                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/221,580
FILING DAME: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DAME: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DAME: 01-APR-1994
ATTORNEY/ACBNT INFORMATION:
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
RICH APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
                                                                                            SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                        FILING DATE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 7; DB 5;
100.0%; Pred. No. 11;
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Best Local Similarity 100.0%; Pred. No. 11,
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,229
REFREENCE/DOCKET NUMBER: 33,229
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 57:
FUNCHAR.
                                                                                                                                                                              STREET: One Liberty Place 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US95/04018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide PCT-US95-04018-57
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: USA
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COUNTRY: USA
ZIP: 19403
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                                                                                                                                                                                                                                                                     ZIP: 19403
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                                                                                                                                                                                                                         STATE: Pe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
CITY: Philadelphia
COUNTRY: USA
ZIP: 19403
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CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                           Query Match 0.9%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches
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0.9%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deblace, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCR-0185
TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION:
                      TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                         , MOLECTLE TYPE: peptide US-08-221-583-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide US-08-221-583-59
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                                                                                                             LENGTH: 15 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            5 QPTPEPS 11
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US-08-221-583-59
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                                                                                                                                                                                           Gaps
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0
                                                                                                                                     Length 490;
                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Seghezzi, Wolfgang
APPLICANT: Seghezzi, Wolfgang
APPLICANT: Shanahan, Frances
APPLICANT: Shanahan, Frances
APPLICANT: McClanahan, Terrill K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                             Query Match
1.0%; Score 8; DB 4;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Scc...
100.0%; Pred. No. J...
... 0; Mismatches
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FILING DATE: 10-DEC-199,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0646
TELECOMMUNICATION INFORMATION:
TRIEDCOMMUNICATION INFORMATION:
TRIEDCOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIT Pall---
; LENGTH: 490
. TYPE: PRT
; CRGANISM: Staphylococcus epidermidis
US-09-134-001C-5116
                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 10, Application US/08999774A; Patent No. 6274312; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-221-583-57; Application US/08221583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 amino acids
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                   150 NDGAVALA 157
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California
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                                                                                                                                                                                                                                                                                                                                                                                       US-08-999-774A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-999-774A-10
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                                                                                                                                                                                                                                                                                                                                                         RESULT 17
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Gaps
                                                                                       NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Heavurer, George A.
TITLE OF INVENTION: THOMON NECTOSIS FACTOR Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STREE: Pennsylvania
COUNTRY: USA
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0
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CAURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25:mdctcMod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 7; DB 1;
100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REPERENCE/POCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58, Application US/08221583
Patent No. 5486595
                                                                                                                                                                                                                                                      ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                    CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 QPTPEPS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPTPEPS 14
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Sequence 5116, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS
TITLE OF INVENTION: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5116
                             APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...332
; SEQUENCE DESCRIPTION: SEQ ID NO: 5477:
US-09-107-532A-5477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFRENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEFHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5477:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.0%; Score 8; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 332 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
US-09-134-001C-5116
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                                    Gaps
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PROTEINS LINKED TO AN
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                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 110
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                                    0; Indels
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CMRPUTER: FILDLY MISS.

COMPUTER: IEM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,166

FILING DATE: 05-UL-1996

CLASSIFICATION DATA:

APPLICATION NUMBER: PCT/FR94/00768

FILING DATE: 24-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PROJECTION DATA:

APPLICATION NUMBER: PROJECTION DATA:

APPLICATION NUMBER: 893/07795

FILING DATE: 25-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 660-106-0 PCT

TELECOMMUNICATION INFORMATION:

MARE: COMMUNICATION INFORMATION:

MATERIALING PROPERTION:

REGISTRATION NUMBER: 660-106-0 PCT

TELECOMMUNICATION INFORMATION:

MATERIALING PROPERTION:

MATERIAL
                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08569166
Patent No. 5830722
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHARLES, LUC
APPLICANT: CHARLES, JEAN-FRANCOIS
APPLICANT: BALLOY, ENERGINE APPLICANT:
TITLE OF INVENTION: CLOSTRIDIUM BIFERMENTANS DNA
TITLE OF INVENTION: BEARING GENES CODING FOR PRO'
TITLE OF INVENTION: INSECTICIDAL ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 7.4; Matches 8; Conservative 0; Mismatches
      Pred. No. 5.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-107-532A-5477
Sequence 5477, Application US/09107532A
; Patent No. 6583275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 34:
      Best Local Similarity 100.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                           178 TNTSNNSNT 186
                                                                                                   249 TNTSNNSNT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 NTSNNSNT 257
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US-08-569-166-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
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APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
CITY: California
                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                           Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 921;
                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: OSMAIN, RACHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                             Query Match 1.1%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.1%; Score 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-646-715-2
; Sequence 2, Application US/08646715
; Patent No. 5637686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
            TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amit-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 921 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tjian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comai, Lucio
                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-582-2
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                                                                                                                                                                                                                                                                                                                                                                      178 TNTSNNSNT 186
                                                                                                                                                                                                                                                                                                                               249 TNTSNNSNT 257
                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: USA
94111-4187
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APPLICANT:
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                                                                                                                                                                                                                                Sequence 143, Application US/09328352

Patent No. 6562958
GRNERAL INFORMATION:
APPLICAMY: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTOS9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                            Gaps
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APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timorhy
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinziarl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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0
                   Length 484;
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                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: CITY CITY CAL Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 941114187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
               Query Match

4.0%; Score 32; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 5.2e-23;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 3,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 4;
Pred. No. 4.8;
                                                                                                                        67 AEQIVIKITDQGYVTSHGDHYHYYNGKVPYDA 98
                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                 46 AEQIVIKITDQGYVTSHGDHYHYYNGKVPYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1994
28-JAN-1994
18: 435
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Patent No. 5534410
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Acinetobacter baumannii
US-09-328-352-6143
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Best Local Similarity 100...
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                                                                                                                                                                                                                         US-09-328-352-6143
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6143
LENGTH: 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-188-582-2
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APPLICANT: JOHNSON, Leslie S.
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.1
       Sequence 182, Application US/09536784
Patent No. 657300.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 45.2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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4.0%; Score 32; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 4.8e-23;
Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                            Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEQIVIKITDQGYVTSHGDHYHYYNGKVPYDA 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REPERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
INFORMATION FOR SEG ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
                                                                                                                                                                          ADDRESSEE: Human Genome Sciel
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: OCT-30-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/09468656A; Patent No. 6582706; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-468-656A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-536-784-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-468-656A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATE Choice: al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                            160 QGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKWELSASELAAAEA 210
                                                                                                                                                                                                                                                                                                                                                                          159 QGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEA 209
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                                                                                                                                                                                                                                                    Length 763;
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                                                                                                                                                                                                                                                                                             0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                            DB 4; Le. 1.2e-41;
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4.0%; Score 32; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 4.8e-23;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                               Query Match 6.4%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 51; Conservative 0; Mismatches
                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 66: US-09-536-784-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPREBRICE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-961-083-182
Sequence 182, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 447 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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US-09-536-784-182
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FILING DATE
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Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNY 90
                 APPLICANT: Adamou, John E.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Vaccine Compositions Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR PRING PAPE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 ENLIPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNY
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Sequence 66, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 819;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%; Score 60; DB 4; Length 819
Best Local Similarity 100.0%; Pred. No. 1.6e-50;
Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 60; DB 4; Le llarity 100.0%; Pred. No. 1.7e-50; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09468656A Patent No. 6582706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Streptococcus pneumoniae
Leslie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICANT: Johnson,
                                                                                                                                                                                                                                                                                                                                                                                    US-09-468-656A-10
                                                                                                                                                                                                                                                                                      SEQ ID NO 10
LENGTH: 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-468-656A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 51; DB 3; Length 763; 100.0%; Pred. No. 1.2e-41; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784 FILING DATE: 30-Oct-1997 CLASSIFICATION: <a href="https://doi.org/10.1007/journal.com/">doi: 10.1007/journal.com/</a>
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
    APPLICATION WINBER: 08/961,083
    FILING DATE: OCT-30-1997
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                           PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34:
TELECOMMUNICATION INFORMATION:
TELEPAN: (301) 309-8504
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 763 amino acids
                                                                    COMPUTER: HP Vectra 48
OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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99.9%; Pred. No. 0
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                                                      LENGTH: 819
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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Best Local Similarity 99.99
Matches 795; Conservative
       NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver.
SEQ ID NO 8
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US-09-468-656A-8
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Patent No. 6582706
GENERAL INFORMATION:
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Paccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-444
CURRENT PALLICATION NUMBER: US/09/468,656A
CURRENT PALLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1998-12-21
                                                                                                                                                                                                                                                                                                              VSNPGTINITNISNNSNINSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQIISRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
WIMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.9%; Sco. 100.0%; Pred. No. v, ... 0; Mismatches
                                  ...ukESEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA.
                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/POCKET NUMBER: PB34C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 796; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-961-083-56
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                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                601 NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLED
                                                                                                                                                                                                                                   601 NRVKGEKRIPLVRLPYMVEHTVEVKKGNLIIPHKDHYHNIKFAMFDDHTYKAPNGYTLED
KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                               481 KEKLVDDLLAFLAFLTHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHSD
                                                                                                                                                                                                                                                                                                 LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADERPVEETPAEPEVP
                                                                                                                                                                                                                                                                                                                                                                                                QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLA
                                                                                                EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Disfette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIL_Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/536,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Michelle S. Marks
REGISTRATION UNMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.9%; Score 795; 100.0%; Pred. No.
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; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-536-784-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-OCt-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Scie.
STREET: 9410 Key West Avenue
CITY: Rockville
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TYPE: amino acid
STRANDEDNESS: single
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Sequence 10, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 21944, A
Sequence 210702, A
Sequence 31029, A
Sequence 37702, A
Sequence 29807, A
Sequence 175, Appl
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Sequence 22113, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 4, Appli
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330,17, A
35, Appli
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Sequence
US-09-171-646-1

US-09-020-116-1

US-09-020-116-1

US-09-328-352-6019

US-09-328-352-6019

US-09-134-01C-4585

US-09-252-991A-2665

US-09-252-991A-26622

US-09-252-991A-26623

US-09-154-602-8

US-09-104-257-4

US-09-102-530-4

US-09-102-530-4

US-09-102-530-4

US-09-102-530-2

US-09-103-522-991A-17702

US-09-252-991A-17702

US-09-252-991A-17702

US-09-252-991A-17702

US-09-252-991A-17702

US-09-252-991A-17702

US-09-118-452A-745

US-09-121-870-103

US-09-121-870-103

US-09-121-870-103

US-09-121-870-103

US-09-131-731A-12

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US-08-961-083-56
; Sequence 56, Application US/08961083
; Sequence 56, Application US/08961083
; GENERAL INFORMATION:
     Sequence 56, Appl
Sequence 56, Appl
Sequence 10, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 66, Appli
Sequence 66, Appli
Sequence 182, App
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6, Appli
6143, Ap
2, Appli
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5477, Ap
5116, Ap
10, Appl
                                                                                                                  ; Search time 24 Seconds
(without alignments)
1712.261 Million cell updates/sec
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PcTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-536-784-56
US-09-468-656A-8
US-09-468-656A-8
US-09-468-656A-10
US-09-468-656A-10
US-09-961-083-66
US-08-961-083-182
US-09-36-784-182
US-09-36-784-182
US-09-36-66-676-67
US-09-36-676-67
US-09-95-67-784-182
US-08-66-67-67
US-08-69-166-34
US-08-69-166-34
US-08-69-166-34
US-08-69-166-34
US-08-69-166-34
US-08-134-10
US-08-134-10
US-08-21-683-57
US-08-21-683-57
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-09-134-001C-5116
-08-999-774A-10
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PCT-US95-04018-59
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US-09-020-116-2
US-09-608-902-2
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                                                                                    - protein search, using sw model
                                                                                                                    2004, 07:31:07
                                                                                                                                                                                                                                                         OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                     US-09-765-271-56
796
1 SYELGLYQARTVKENNRVSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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                                                                                                                    October
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Perfect score:
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                                                                                                                  Run on
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No.
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SEQUENCE FROM N.A.
STRAIR=MLS / ATCC 700699, and N315;
MEDLINE=MLS / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuri L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 1, 2004, 07:32:52
      WCBI_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                         Jancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 IIEDTGD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Job time : 24 secs
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                                                                                                                                                                                                            aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                     o;
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0
                   Gaps
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 23877;
MEDLINE=95020551; PubMed=7934842;
Hagege J., Pernodet J.L., Friedmann A., Guerineau M.;
"Mode and origin of replication of pSAM2, a conjugative integrating element of Streptomyces ambofaciens.";
Mol. Microbiol. 10:799-812(1993).
-! SIMILARITY: Belongs to the NUDIX hydrolase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcription elongation factor greA (Transcript cleavage factor
                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                     Indels
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100.0%; Pred. No. 44;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 AA; 16689 MW; 8EC2EE99D272D656 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GREA OR SAV1610 OR SA1438 OR MW1560.
Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N15), and
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                     .;
0
                                                                                                                                                                                                                                                                                               Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1889;
                                                                                                                                                                                      01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 40, Last annotation update)
MutT-like protein (ORF154).
 Pred. No. 42;
                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUDIX BOX
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InterPro, IPR000086, NUDIX_hydrolase.
Pfam, PF00293, NUDIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00502; NUDIXFAMILY. PROSITE; PS00893; NUDIX; 1.
100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                   Streptomyces ambofaciens.
Plasmid pSAM2.
                   7; Conservative
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                               303 GVAVPHG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 LTPDEVS 120
                                                                          59 GVAVPHG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 LIPDEVS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid; Hydrolase.
   Best Local Similarity
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1D GREA STAAM

AC 099TN9;
DT 28-FEB-2003
DT 28-FEB-2004
DE Transcription
DE Transcription
DE GREA OR SAV1:
GN GREA OR SAV1:
CS Staphylococci
OS Staphylococci
OC Bacteria; Fi
                                                                                                                        RESULT 24
MUTT STRAM
ID MUTT STRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                          P32091;
                 Matches
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                                                                                                                                                                                                                                           adjusted 359:1819-1827(2002).

-I-FUNCTION: Necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have the property of trapping a certain fraction of elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as greA or greB allows the resumption of elongation from the new 3'terminus. GreA releases sequences of 2 to 3 nucleotides (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Coiled coil; Complete proteome. DOMAIN 4 76 COILED COIL (POTENTIAL). SEQUENCE 158 AA; 17743 MW; EC3B0F0B6238A107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
STRAIN=MW2;
MEDLINE=22040717; PubMed=12044378;
MEDLINE=22040717; PubMed=12044378;
Maba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Baba T., Takeuchi F., Kuroda H., Cui L., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                              Nagai Y., Iwama N., Asano K., Naimi 1., Auroua ..., ... Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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100.0%; Pred. No. 45;
cive 0; Mismatches
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InterPro; IPR006359; GreA.
InterPro; IPR001437; GreA.GreB.
Pfam: PF0127; GreA.GreB. 1.
Pfam: PF013449; GreA.GreB. N.
TGRODm: PD00494B; GreA.GreB. N.
TGRFAMS; TIGR01462; GreA.GreB. 1.
PROSITE; PS00829; GREAB 1; 1.
PROSITE; PS00830; GREAB 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP003362; BAB57772.1; --
EMBL; AP003134; BAB42702.1; --
EMBL; AP004827; BAB95425.1; --
PIR; AB9943; AB9943.
HSSP; P21346; 1GRU.
SWISS-2DPAGE; Q99TN9; STAAN.
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hes 7; Conservative
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FROM N.A.
                                                                                                                                                                                                                                                    Mau B., Shao Y.;
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           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTVA ECOLI STANDARD; PRT; 148 AA.
P32155; P76776;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PTS system, fructose-like-1 IIA component (Phosphotransferase enzyme III, A component) (EC 2.7.1.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                         Podowski R.M., Naeslund A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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0
119 119 BY SIMILARITY.
34 34 N-LINKED (GLCNAC. .) (PARTIAL).
124 AA; 13711 MW; 9435EF532420F852 CRC64;
                                                                                                                                                                                                                                                                                                                     Andersson S.G.E., Zomerodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin mitochondria.";
                                                                                                                                                                                                                                           Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
                                          0.9%; Score 7; DB 1; Length 124;
100.0%; Pred. No. 36;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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100.0%; Pred. No. 41;
.ve 0; Mismatches
                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Hypochetical protein RP082.
                                                                                                                                                                143 AA.
                                                                                                                                                                                                                                                                Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ235270; CAA14552.1; -.
PIR; A71717; A71717.
Hypothetical protein; Complete proteome.
SEQUENCE 143 AA, 16939 MW; 57637C7A6
                                                                                                                                                                                                                                                                                                                    MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Nature 396:133-140(1998).
                                                                  Conservative
                                                                                                                                                                STANDARD;
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                                                                                      785 SNPSSVS 791
                                                                                                           SNPSSVS 21
                                                      Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                            STRAIN=Madrid E;
                                                                                                                                                                                                                                                                            NCBI_TaxID=782;
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                                                                                                                                                               Y082 RICPR
Q9ZE65;
                                                                                                            15
  ACT_SITE
           CARBOHYD
                      SEQUENCE
                                             Query Match
                                                                                                                                           RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein histidine + sugar phosphate.
-| histidine + COATION: Cytoplasmic (Probable).
-| SUBCELLUIAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=54290319; PubMed=8019415;
Reizer J., Michotey V., Reizer A., Saier M.H. Jr.;
"Novel phosphotransferase system genes revealed by bacterial genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 81 AND 104-108.
STRAIN=K1Z / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MG1655;
MEDLINE-9334769; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
Finallysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes: ";
Nucleic Acids Res. 21:3391-3398(1993).
                                  Moralejo P., Egan S.M., Hidalgo E.F., Aguilar J.; "Sequencing and characterization of a gene cluster encoding the enzymes for L-rhamnose metabolism in Escherichia coli."; J. Bacteriol. 175:5585-5594(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation; Complete proteome.

MOD RES 64 64 PHOSPHORYLATION (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00372; PTS ELIA 2; 1.
Phosphotransferase system; Sugar transport; Transferase;
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QSGE -> KXZ (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L19201; AAB03033.2; --
EMBL; AE000465; AAC76882.1; --
PIR; D48649; D48649.
ECGGene; EG11864; frvA.
InterPro; IPR002178; PTS_EIIA_2.
InterPro; IPR00415; PTS_IIA_2.
Pfam, PF00359; PTS_EIIA_2; IPRODO:
ProDom; PD001689; PTS_EIIA_2; ITREPOMS; TIGR00848; FTS_EIIA_2; ITREPEMS; TIGR00848; FTVA; ITREPAMS; TIGR00848; FTVA; ITREPAMS; TIGR00848; FTVA; ITREPAMS; TIGROOR48; FTVAX; TIGROOR48;
MEDLINE=93374854; PubMed=8396120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16093 MW;
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Protein Sci. 3:440-450(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60472; CAA43004.1; -.
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0.9%; Score 7; DB 1; Length 148;

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Complete proteome.
SEQUENCE 121 AA;
                                               AE015218;
                                                                          AE015284;
                                  AE015180;
                    AE015170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNASE1 OR RNS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNP_ANTAM
ID _ RNP_ANTAM
                                                                                                                                                                                                                                                                                                                                                                                         70
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                                                                                                      EMBL;
EMBL;
EMBL;
                                            EMBL;
EMBL;
                                                                        EMBL;
EMBL;
                                EMBL;
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     Пb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002).
-!- FUNCTION: Involved in the transposition of the insertion sequence IS2 (By similarity).
          EMBL; D90779; BAA15019.1; ALT_INAT.

EMBL; D90839; BAA15019.1; ALT_INIT.

EMBL; D908050; BAA16005.1; ALT_INIT.

EMBL; D908051; BAA16013.1; ALT_INIT.

EMBL; D90852; BAA1603.1; ALT_INIT.

Exceeden; EG40003; insc.

InterPro; IPR002514; Transposase 8.

Fran; PF01527; Transposase 8; 1.

Transposable element; Transposation; DNA-binding; DNA recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin C., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin G., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
11-OCT-2003 (Rel. 42, Last sequence update)
12 Transposase insC for insertion element is2.
13 Transposase insC for insertion element is2.
14 (INSC1 OR SF0245) AND (INSC2 OR SF0879) AND (INSC3 OR SF1165) AND (INSC3 OR SF1165) AND (INSC3 OR SF1165) AND (INSC3 OR SF1165) AND (INSC3 OR SF2011) AND (INSC3 OR SF3413) AND (INSC3 OR SF3312) AND (INSC3 OR SF3313) AND (INSC3 OR SF3313) AND (INSC3 OR SF3313) AND (INSC3 OR SF3313) AND (INSC3 OR SF3385) AND (INSC3 OR SF3387) AND (INSC3 OR SF3387) AND (INSC3 OR SF3387) AND (INSC21 OR SF3185) AND (INSC21 OR SF4185).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                      Length 121
                                                                                                                                                           L -> F (IN B1997).
; 59431E5C452E067A CRC64;
                                                                                                                                                                                                    0.9%; Score 7; DB 1;
100.0%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              121 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE015060, AAN41906.1, ALT INIT.
EMBL, AE015116, AAN42511.1; ALT INIT.
EMBL, AE015123, AAN42562.1, ALT INIT.
EMBL, AE015125, AAN4258.1, ALT INIT.
EMBL, AE015133, AAN42676.1, ALT INIT.
EMBL, AE015133, AAN42676.1, ALT INIT.
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                          VARÎANT 34 34 L
SEQUENCE 121 AA; 13452 MW;
D90778; BAA15013.1;
                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                            202 ASELAAA 208
                                                                                                                                                                                                                                                                                    ASELAAA 76
                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shigella flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                           INSC SHIFL
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                        P59444;
                                                                                                                                                                                                                                                                                                                                RESULT 20
INSC_SHIFL
 EMBL;
                                                                                                                                                                                                                                Matches
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Pfam; PF01527; Transposase 8; 1. Transposate at Transposable element; Transposition; DNA-binding; DNA recombination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The first of the properties of
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U-P
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AA; 13452 MW; 59431E5C452E067A CRC64;
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100.0%; Pred. No. 35;
iive 0; Mismatches
                                                                                                                                                                                                                                                                        ALT INIT.
                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE015387; AAN45285.1; ALT INIT.
EMBL, AE015394; AAN45310.1; ALT_INIT.
EMBL, AE015405; AAN45422.1; ALT_INIT.
EMBL, AE015418; AAN45522.1; ALT_INIT.
EMBL, AE015427; AAN45606.1; ALT_INIT.
INITERPRO; IPR002514; Transposase_8
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TISSUE=Pancreas;
MEDLINE=80075014; PubMed=513141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                     AE015311; AAN44465.1;
AE015351; AAN44892.1;
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NCBI_TaxID=9891;
                                                                                                                     AAN43556.1;
                                                                                                                                                               AAN44112.1;
AAN44187.1;
                                                                                                                                                                                                                                                   AE015301; AAN44359.1;
                                                                                                                                                                                                                                                                                                                                                                     AE015359; AAN44970.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.9
Best Local Similarity 100.
Matches 7; Conservative
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MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Aiba H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horluchi T., A460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KI2 // MGIG55,

MEDLINE=97426617; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=KL2;
MEDLINE=97251357; PubMed=9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Alba H., Raba H., Kashimoto K., Kimura S., Kitakawa M., Itch T., Kasai H., Kashimoto K., Mixobuchi K., Mori H., Moromura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Moromura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Gshima T., Salto N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
Yamamoto Y., Horiuchi T.;
Yamamoto Y., Horiuchi T.;
Yamamoto Y., Boriuchi T.;
Yamapoto Y., Boriuchi T.;
Yamamoto Y., Horiuchi T.;
Yamamoto Y., Boriuchi T.;
Yamamoto Y., Horiuchi T.;
                                                Ronecker H.J., Rak B., "Genetic organization of insertion element IS2 based on a revised
                                                                                                                                                                                                                                                                                                                                                                                                            "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                          STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 23:2105-2119(1995).
                             MEDLINE=88137965; PubMed=2830172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; V00279; CAA23542.1; -.
                                                                                                                                 nucleotide sequence.";
Gene 59:291-296(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gregor J., Davis
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                          Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from pre-tRNA to produce the mature 5 terminus. It can also cleave other RNA to produce the mature 5 terminus. It can also cleave other RNA substrates such as 4.5S RNA. The protein component plays an auxiliary but essential role in vivo by binding to the 5'-leader sequence and broadening the substrate specificity of the
                                 Ribonuclease P protein component (EC 3.1.26.5) (RNaseP protein) (RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extra-nucleotide from tRNA precursor.
SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and protein subunit (By similarity).
SIMILARITY: Belongs to the rnpA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribozyme (By similarity).
CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'
                                                                                                                                                                                                                                                                                                                                                                                      Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M., "Genome-based analysis of virulence genes in a non-biofilm-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO0188; rnpA; 1. -
PROSITE; PS00648; RIBONUCLEASE_P; 1.
Hydrolase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSC ECOLI STANDARD; PRT; 121 AA.
P19776: 007999; 008019; 008019; P76357; P77346;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-3001 (Rel. 40, Last annotation update)
16-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AA; 13484 MW; 106B2592C8400F18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis strain (ATCC 12228).";
Mol. Microbiol. 49:1577-1593(2003).
                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Staphylococcus.
   10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF 00227; -; 1.
InterPro; IPR000100; Ribonuclease P.
Pfam; PF00825; Ribonuclease P; 1.
ProDom; PD003629; Ribonuclease P; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE016752; AA006061.1; -.
                                                                                                                                            Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 7; Conservative
                                                                      protein) (Protein C5).
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                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 12228;
PubMed=12950922;
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                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                        1014003; AAA97168.1; ALT_INIT.
1028377; AAA89212.1; ALT_INIT.
1028375; AAA83943.1; ALT_INIT.
AB000237; AAC73463.1; ALT_INIT.
AB000237; AAC74485.1; ALT_INIT.
AB000237; AAC7688.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000369; AAC75900.1; -. -
EMBL; AE000386; AAC76080.1; -.
EMBL; AE000498; AAC77228.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

Escherichia coli

ECOLI

Matches

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[1] SEQUENCE FROM N.A.

NCBI\_TaxID=562;

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Gaps

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Indels

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Pred. No. 30;
0; Mismatches
    100.08;
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                                                                                                                                                                                                                                                                                                                                        Hypothetical protein HI1436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995)
    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
                                                                     404 PSETVKN 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AAEAFLS 213
                                                                                                               PSETVKN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 AAEAFLS 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HI1436; -
                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                    HI1436
                                                                                                                                                                                                        YOCC HAEIN
                       Matches
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  oved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urealyticum.";
Nature 407:757-762(2000).
-1- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
NCBL_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen B.Y., Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                    Redox-active center; Electron transport.
DISULFID 25 28 REDOX-ACTIVE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 7; DB 1; Length 101
100.0%; Pred. No. 30;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete sequence of the mucosal pathogen Ureaplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 101
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HAMAP; ME 00185; -: 1.

INTERTO; IPRO00307; Ribosomal S16.

Pfam; PF00886; Ribosomal S16; I.

Probom; PD003791; Ribosomal S16; I.

TICRPAMS; TICR00002; S16; I.

PROSITE; PS00732; RIBOSOMAL S16; PALSE NEG.

Ribosomal protein; Complete proteome.

SEQUENCE 101 AA; 11297 MW; FED91E1AB36CBF45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       52 52 N -> D (IN REF. 3).
101 AA; 11261 MW; 30557E19BF33E9BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FRBS-2003 (Rel. 41, Last annotation update)
RPSP OR RPSIG OR UU568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AA.
modified and this statement is not removed.
                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                              HSSP, P35754; IJHB.
GeneDB SPombe; SPAC4F10.20; -..
InterPro; IPR002109; Glutaredoxin.
InterPro; IPR006663; Thioredox dom2.
Pfam; PF00462; glutaredoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Serovar 3; MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                              PRINTS; PR00160; GLUTAREDOXIN.
PROSITE; PS00195; GLUTAREDOXIN; 1.
                                                                                                        EMBL; AB015167; BAA28750.1; -. EMBL; AF192764; AAF19628.1; -. EMBL; AF121275; AAD25391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE002155; AAF30982.1; -.
HSSP; P80379; 1EMW.
                                                                                      EMBL; 298980; CAB11722.1; -.
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Matches 7; Conservative
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                                                                                                                                                                PIR; T38824; T38824.
HSSP; P35754: 1.THD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              461 NSDFQAL 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 NSDFOAL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS16 UREPA
ID RS16 UREPA
DT COPPEDITOR
DT 16-OCT-
DT 28-FEB-
DE 30S TIME
ON UREAPING
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ON UREAPING
RA CASSOLIEN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO THE N-TERMINAL OF B.CAROTOVORA EXCENZYME REGULATION REGULON ORF1. THE C-TERMINAL PART IS COLINEAR WITH YQCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Genehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 106;
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Pfam; PF04287; DUF446; 1.
PIRSF; PIRSF006257; UCP006257; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 106 AA; 112273 MW; 0955920EBD63228C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
5. 31;
YQCC_HAEIN STANDARD; PRT; 106 AA. Q57152; 005061; 15-JUL-1998 (Rel. 36, Created) 28-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
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(Rel. 42, Last sequence update)
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100.0%; Pred. No. 31;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
RNPA_STAEP
ID RNPA_STAEP
AC QGCMA_4;
DT 10-OCT-2003 (;
DT 10-OCT-2003 (;
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101 AA.

PRT;

STANDARD;

SCHPO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barnes P.F., Mehra V., Rivoire B., Fong S.J., Brennan P.J., Voegtline M.S., Minden P., Houghten R.A., Bloom B.R., Modlin R.L.; "Immunoreactivity of a 10-kDa antigen of Mycobacterium tuberculosis."; J. Immunol. 148:1835-1840(1992).

-I. FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses the ATPase activity of the latter.

-I. SUBJUNIT: Heptamer of 7 subunits arranged in a ring (By
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                 STRAIN-CDC 1551 / Oshkosh;

MEDLINE=22206494; PubMed=12218036;

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Pleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,

Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,

Bishai W., Jacobs W.R. Jr., Vonter J.C., Fraser C.M.;

"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rausite; ESOU681; CHAPERONINS CPN10; 1.
Chaperone; Antigen; Heat shock; Complete proteome; 3D-structure.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the großs chaperonin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA; 10673 MW; 1DD128E75CF19AF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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100.0%; Pred. No. 30;
ttive 0; Mismatches
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HAMAP; MF_00580; -; 1.
InterPro; IPR001476; Chaprnin_Cpn10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00166; cpn10; 1.
PRINTS; PR00297; CFAPERONIN10.
PRODOW: PD000566; Chaptrin Cpn10; 1.
PROSITE; PS00681; CHAPERONINS_CPN10;
                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92176646; PubMed=1371791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X60350; CAA42908.1; -.
EMBL; M25258; AAA25340.1; -.
EMBL; X13739; CAA32003.1; -.
EMBL; Z77165; CAB01005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE007158; AAK47865.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S01381; BVMYBA.
PDB; 1HX5; 08-AUG-01.
PDB; 1P3H; 15-JUL-03.
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Best Local Similarity
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGR; MT3527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
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EMBL;
EMBL;
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                                                                                                                                                                                                             SEQUENCE FROM N.A. Cho Y.-W., Kim H.-G., Lim C.-J.; Cho Y.-W., Kim H.-G., Lim C.-J.; "Isolation and expression of the genomic DNA encoding thioltransferase
                                                                                                                                                                Kim H.-G., Cho Y.-W., Park E.-H., Lim C.-J.;
"Characterization of cDNA encoding thioltransferase (glutaredoxin)
                                                                                                                                                                                                                                        (Glutaredoxin) from Schizosaccharomyces pombe.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                  from Schizosaccharomyces pombe.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                      Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the glutaredoxin family.
                                  (Rel. 41, Last annotation update)
                        Last sequence update)
                                                             Schizosaccharomyces pombe (Fission yeast).
     036032; 09US58;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq.
                                                   GRX1 OR SPAC4F10.20.
                                                                                        Schizosaccharomyces.
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=4896;
                                           Glutaredoxin 1
                                  28-FEB-2003
                                                                                                                              Kawamukai
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Gaps

.; 0

0; Indels

7; Conservative

Matches

605 GEKRIPL 611 GEKRIPL 60 ·;

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HSSP; P05380; 1AON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Erdmann;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walker L.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHIO MYCTU
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
CH10 MYCTU
CH10 MYCTU
DT 01-MAR-
DT 30-MAR-
DT 10-OCT-
D
                                                                                                                                                                                                                                                                                                                 Matches
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                      noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
10 kDa chaperonin (Protein Cpnl0) (groES protein) (Immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AF2122/97;

MEDLINE=22709107; PubMed=12788972;

Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,

Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,

Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,

Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;

"The complete genome sequence of Mycobacterium bovis.";

Proc. Natl. Acad. Sci. U.S.A. 100:1877-7882(2003).

-! FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses

the ATPseas activity of the latter.

-! SUBUNIT: Heptamer of 7 subunits arranged in a ring (By
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Immunogenic protein MPB57 from Mycobacterium bovis BCG: molecular cloning, nucleotide sequence and expression."; FEBS Lett. 240:115-117(1988).
    is in
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MEDLINE=89052868; PubMed=3056744;
Yamaguchi R., Matsuo K., Yamazaki A., Nagai S., Terasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    as its content
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                  Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                      4BDE6021B7DF8032 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterineae; Mycobacteriaceae; Mycobacterium (VCBI_TaxID=1765;
                                                                                                                                                                                                                                                               0.9%; Score 7; DB 1;
100.0%; Pred. No. 22;
iive 0; Mismatches
                    modified and this statement is not removed. entities requires a license agreement (See h
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non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                               Interpro: IPR008203; DUF104.
Pfam; PF01954; DUF104; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 70 AA; 8009 MW; 4BDE6021B7I
                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GROS OR GROES OR MOPB OR MB3452C.
                                                                                                         EMBL; AJ248285; CAB49786.1; -. PIR; A75134; A75134.
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EMBL, M35389; AAA225365.1; -.
EMBL, BX248346; CAD95639.1; -.
PIR; S01784; BVMY7B.
                                                                                                                                                                                                                                                        Query Match 0.9 Best Local Similarity 100. Matches \begin{pmatrix} \gamma_i \end{pmatrix} Conservative
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                                                                                                                                                                                                                                                                                                                                                      478 STNKEKL 484
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STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE=89016584, PubMed=2902558,

Baird P.N., Hall L.M., Coates A.R.M.;
"A major antigen from Mycobacterium tuberculosis which is homologous to the heat shock proteing groß from E. coli and the htpA gene product of Coxiella burneti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-93219332; PubMed-7681982; Rong T.H., Coates A.R.M., Butcher P.D., Hickman C.J., Shinnick T.M.; "Mycobacterium tuberculosis expresses two chaperonin-60 homologs."; Proc. Natl. Acad. Sci. U.S.A. 90:2608-2612(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P09621;
30-MAY-1099 (Rel. 10, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10 Nb chaperonin (Protein Cpn10) (groß protein) (BCG-A heat shock grosin) (10 kba antigen).
GROS OR GROES OR MOPB OR CPN10 OR RV3418C OR MT3527 OR MTCY78.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Mycobacterium tuberculosis BCG-a protein has homology with the Escherichia coli GroES protein.";
Nucleic Acids Res. 17:1254-1254(1989).
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Shinnick T.M., Plikaytis B.P., Hyche A.D., van Landingham R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90095443; PubMed=2480990;
Baird P.N., Hall L.M.C., Coates A.R.M.;
"Cloning and sequence analysis of the 10 kba antigen gene of
Mycobacterium tuberculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                   LAVVS -> VGRRF (IN REF. 1).
1DD128E75CF19AF7 CRC64;
                                                                                                                                                                                                                                                                                                                                             Length 99;
HAMAP, MF 00580, -; 1.

Interpro; IPR001476; Chaprnin_Cpn10.

Pfam; PR00166; cpn10, 1.

PRINTS; PR00297; CHAPERONIN10.

PROSITE; PS00681; CHAPERONINS CPN10; 1.

PROSITE; PS00681; CHAPERONINS CPN10; 1.

CAMPERONE; Antigen; Heat shock; Complete proteome.

CONFILCT 94 98 LAVVS -> VGRRF (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                    0.9%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gen. Microbiol. 135:931-939(1989).
                                                                                                                                                                                                                                                                                  99 AA; 10673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.

ses 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   605 GEKRIPL 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 GEKRIPL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Komoo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komoo H., Adachi J., Fukuda S., Aizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ashbir D., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehbush J., Schriml L., K., Okido T., Furunto M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bolinga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Loen B., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannia H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wannia M., Wanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: May form a homodimer or a heterodimer with PPL.
-!- SUBCELLULAR LOCATION: COLOCALIZED WITH DSP AT DESMOSOMES AND ALONG INTERMEDIATE FILAMENTS (BY SIMILARITY).
-!- SIMILARITY: Contains 7 plectin repeats.
-!- SIMILARITY: Contains 1 spectrin repeat.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
-!- FUNCTION: Component of the cornified envelope of keratinocytes.
May link the cornified envelope to desmosomes and intermediate
                                     Omega-hydroxyceramide glutamate ester (Probable).
Omega-hydroxyceramide glutamate ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                 Length 2033;
                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Envoplakin (p210) (210 kDa cornified envelope precursor).
                                                                                                                                                           0; Indels
                                                                             2033 AA; 231616 MW; B8DC6E2B52221938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maatta A., Ruhrberg C., Watt F.M.;
"Structure and regulation of the envoplakin gene.";
J. Biol. Chem. 275:19857-19865(2000).
                                                                                                                   Score 8; DB 1;
                                                                                                                                                                                                                                                                                                                                           PRT; 2035 AA.
                                                                                                                                        No. 40;
                                                                                                                           100.0%; Pred. ...
                       (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1860-2035 FROM N.A.
STRAIN-C57BL/6J; TISSUE-Pancreas;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20347896; PubMed=10747979;
                                                                                                                   1.0%;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                       1607
                                                                                                                                                                                                  731 LKEAEVLL 738
                                                                                                                                                                                                                                        87 LKEAEVLL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   musculus (Mouse)
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
871
                                       1607
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                                     LIPID
  LIPID
                                                                                                                                                             Matches
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                       (See http://www.isb-sib.ch/announce/
and for commercial
                                                                                                                                                                                                                                                                                                                       MGD; MGI:107507; Evpl.
InterPro; IRMO1101; Plectin repeat.
InterPro; IRMO2011; Spectrin.
Pfam; PF00481; Plectin; 3.
Pfam; PF00481; Spectrin; 2.
SMART; SM00250; PLEC; 8.
Keratinization; Repeat; Coiled coil; Cytoskeleton; Structural protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENTRAL FIBROUS ROD DOMAIN.
GLOBULAR 2.
4 X 4 AA TANDEM REPEATS OF K-G-S-P.
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0
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  Usage
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical UPF0165 protein PYRAB08720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 AA.
  modified and this statement is not removed.
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cive 0; Mismatches
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PLECTIN 4.
PLECTIN 5.
                          entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                              EMBL; AJ309317; CAC38864.2; -.
EMBL; AJ319607; CAC38864.2; JOINED.
EMBL; AJ319609; CAC38864.2; JOINED.
EMBL; AJ319610; CAC38864.2; JOINED.
EMBL; AJ319610; CAC38864.2; JOINED.
EMBL; AJ319611; CAC38864.2; JOINED.
EMBL; AJ319613; CAC38864.2; JOINED.
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MIM; 601590;
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                                                                                                                                                                                                                            J. Bacteriol. 184:5479-5490(2002).
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN CHROMOSOME STRUCTURE AND PARTITIONING. ESSENTIAL FOR CHROMOSOME PARTITION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Envoplakin (210 kDa paraneoplastic pemphigus antigen) (p210) (210 kDa
                     MEDLINE=22206494; PubMed=12218036; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L., Delcher A., Utterback T., Weidmu J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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BUDILINE=26326676, PubMed=8707850;

RUhrberg C., Hajibaqheri M.A.N., Simon M., Dooley T.P., Watt F.M.;

"Envoplakin, a novel precursor of the cornified envelope that has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the SMC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z74697; CAA98982.1; ALT_INIT.
EMBL; AE007121; AAK47317.1; --
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J. Cell Biol. 134:715-729(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: May form a homodimer or a heterodimer with PPL. SUBCELLULAR LOCATION: COLOCALIZED WITH DSP AT DESMOSOMES AND ALKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00681; Plectin; 3. SMART; SM00250; PLEC; 8. Keratinization; Repeat; Coiled coil; Cytoskeleton; Structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: During differentiation of epidermal keratinocytes. PTM: Substrate of transglutaminase. Some glutamines and lysines are cross-linked to other envoplakin molecules, to other proteins such as keratin, desmoplakin, periplakin and involucrin, and to
                                                                                                                                                                                                   the TOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Exclusively expressed in stratified squamous
                                                                Risk J.M., Ruhrberg C., Hennies H.-C., Mills H.S., Di Colandrea T.,
Evans K.E., Ellis A., Watt F.M., Bishop D.T., Spurr N.K.,
Stevens H.P., Leigh I.M., Reis A., Kelsell D.P., Field J.K.,
"Envoplakin, a possible candidate gene for focal NEPPK/esophageal
cancer (TOC): the integration of genetic and physical maps of the T
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98316349; PubMed=9651377;
Marekov L.N., Steinert P.M.;
"Ceramides are bound to structural proteins of the human foreskin epidermal cornified cell envelope.";
J. Biol. Chem. 273:17763-17770(1998).
-!-FONCTION: Component of the cornified envelope of keratinocytes. May link the cornified envelope to desmosomes and intermediate filaments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omega-hydroxyceramide glutamate ester (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 X 4 AA TANDEM REPEATS OF K-G-S-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipids like omega-hydroxyceramide.
SIMILARITY: Contains 7 plectin repeats.
SIMILARITY: Contains 1 spectrin repeat
SIMILARITY: Belongs to the plakin or cytolinker family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CENTRAL FIBROUS ROD DOMAIN.
GLOBULAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COILED COIL (POTENTIAL)
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GO: GO:0005198; F:structural molecule activity; T;
GO; GO:0008544; P:epidermal differentiation; TAS.
InterPro; IPR001101; Plectin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLOBULAR 1.
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PLECTIN 2.
PLECTIN 3.
PLECTIN 4.
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SEQUENCE FROM N.A. MEDLINE=99339988; Pubmed=10409435;
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EMBL; U72849; AAD00186.1; -...
EMBL; U72843; AAD00186.1; J. JOINED.
EMBL; U72846; AAD00186.1; JOINED.
EMBL; U72846; AAD00186.1; JOINED.
EMBL; U72848; AAD00186.1; JOINED.
EMBL; U72848; AAD00186.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERMEDIATE FILAMENTS.
                                                                                                                                                                                                                                  region on 17q25.";
Genomics 59:234-242(1999).
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1135
1226
1713
1713
1855
1893
1969
2007
657
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Backova D., Botchan M.R., Bouck J., Broketein P., Brothievo S., Burkova D., Botchan M.R., Bouck J., Broketein P., Brothier P., Charler P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cahery J.M., Cawley S., Dahke C., Davenport L.B., Davies P., Caper D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Borbin S., Capielian A.E., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Angelistan A.E., Garral J.H., Gu Z., Kernison J.R., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Alaris M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A., Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A., Liu J.H., Li Z., Liang Y., Lin X., Liasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntcsh T.C., McLeod M.P., McCherson D., Markin B., Murphy L., Muzny D.M., Nalson D.L., Rainent B., McIntan G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rainert K., Remington K., Sampson M., Stupski M.P., Santh T., Sante R., Spier E., Spradling A.C., Stapleton M., Stupski M.P., Santh T., Santh T., Wallson D.Y., Wang A.H., Wang S., Yao, S., Yao, Yang S., Yao, W., Williams S.M., Woodage T., Worlex E., Wang A.H., Wang S., Yao, Yao, R., Zhong K., Zhong K., Zhong S., Zh 

SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY. PARTIAL

rissue=Embryo;

\*\*MEDLINE=98198453; PubMed=9531534; Steneberg P., Englund C., Kronhamn J., Weaver T.A., Samakovlis C.; Steneberg P., Englund C., Kronhamn J., Weaver T.A., Samakovlis C.; Steneberg P., Englund C., Kronhamn J., Weaver T.A., Samakovlis C.; Translational readthrough in the hdc mRNA generates a novel branching in inhibitor in the Drosophila trachea."; Genes Dev. 12:956-967(1998).

-!- PUNCTION: Required for imaginal cell differentiation, may be involved in hormonal responsiveness during metamorphosis. Involved in an inhibitory signaling mechanism to determine the number of cells that will form unicellular sprouts in the trachea. Regulated by transcription factor esg. The longer hdc protein is completely functional and the shorter protein carries some function.

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- TISSUE SPECIFICITY: Expressed in all imaginal cells of the embryo and larvae. Expressed in a subset of tracheal fusion cells from stage 14 to the end of embryogenesis in metameres 2-9, lateral

trunk and ventral anastomoses. MISCELLANBOUS: Readthrough of the terminator UAA occurs between codons for Ala-650 and His-652. Readthrough is not always suppressed as the shorter protein is more abundant. CAUTION: Ref.2 sequence differs from that shown due to erroneous

gene model prediction.

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EMBL, AE003773; AAF57033.1; ALT\_SEQ. FlyBase; FBgn0010113; hdc. EMBL; Z50097; CAA90425.1; -EMBL; Z50097; CAB58233.1;

GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0007430; P:terminal branching of trachea, cytoplasmic . . .; NAS.
Developmental protein.
CHAIN

> PACCR	Gaps
GGS -	0;
OTEIN. ); 1): 1): 1): 1): 1): 1): 1): 1): 1): 1):	0; Indels
HEADCASE SHORT PROTEIN.  POLY-GLY.  POLY-GLY.  POLY-GLY.  POLY-GLN.  GLN-RICH.  GLN-RICH.  POLY-SER.  POLY-SER.  POLY-SER.  POLY-SER.  POLY-SER.  POLY-SER.  POLY-SER.  POLY-SER.  H -> P (IN REF. 1).  PT -> SN (IN REF. 1).  SGVLOTSALARTSOILENTNNVLGLDLRARAGS ->  ROWNPLSATESITEMSNUTGHORDLRARAGS ->  BY -> HD (IN REF. 1).  SY -> HD (IN REF. 1).  T -> S (IN REF. 1).  D -> E (IN REF. 1).  T -> S (IN REF. 1).  T -> S (IN REF. 1).  T -> S (IN REF. 1).  S -> S (IN REF. 1).  S -> S (IN REF. 1).  My, BYEBLIARADDLBYRY CRC64;  SCORE B; DB 1; Length 1080;  Pred. NO. 23:	
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650 218 227 395 395 395 769 815 815 891 970 1091 224 244 310 342 310 342 343 343 343 343 343 343 343 343 343	rat
22122 22122 22123 23843 23843 2486 2486 2486 6491 1067 1067 1067	Cons
CHAIN  DOMAIN  DOMAIN  DOMAIN  219  DOMAIN  219  DOMAIN  343  DOMAIN  POMAIN  POMAIN  POMAIN  R87  DOMAIN  R87  DOMAIN  R87  DOMAIN  R87  CONFLICT  CONFLICT	Matches 8;
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STANDARD; 836 TNTNTSNN 843 SMC\_MYCTU Q10970; SMC\_MYCTU RESULT 9 g

247 TNTNTSNN 254

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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; STRAIN=H37Rv; Cobbe N., Heck M.M.S.; "Phylogenetic analysis of SMC proteins."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. Corynebacterineae; Mycobacteriaceae; Mycobacterium 01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
SMC OR RV2922C OR MT2990 OR MTCX338.11C. Mycobacterium tuberculosis. SEQUENCE FROM N.A. NCBI\_TaxID=1773;

MEDINE=80295987; PubMed=9634230; MEDINE=80295987; PubMed=9634230; MEDINE=80295987; PubMed=9634230; MEDINE=80295987; PubMed=9634230; MEDINE=8029887; PubMed=R., Barchill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglnefer K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Backock K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Hornsby T., Jagels K., Kroph A., Rolandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulaton J.E., Taylor K., Whitehead S., Barrell B.G.; Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; SEQUENCE FROM N.A. 

Nature 393:537-544 (1998).

SEQUENCE FROM N.A.

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Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., Hayashizaki Y., Vohnon-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Kamiya A., Meyers C., Nakajima M., Wallender E.K., Wong C., Yamamura Y., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryo;
MEDLINE=96171720; PubMed=8575315;
Weaver T.A., White R.A.;
"Headcase, an imaginal specific gene required for adult morphogenesis in Drosophila melanogaster.";
Development 121:4149-4160(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132; Adams C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                Chane-Favre L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
Sarazin B., Tonella L., Marques K., Paesano S., Chane-Favre I
Heller M., Sanchez J.-C., Hochstrasser D.F., Thiellement H.;
Unpublished observations (SEP-2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE 861 AA; 96615 MW; 9F53F0BFF013D673 CRC64;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
Headcase protein [Contains: Headcase short protein].
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                                                                                                                                                                                     Science 302:842-846(2003).
                                                                                                                                                                                                                            IDENTIFICATION ON 2D-GELS.
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MEDLINE=22954850; PubMed=14593172;
Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
Soutbwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20083487; PubMed=10617197; MEDLINE=20083487; PubMed=10617197; Inn X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Sonerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis
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PROSITE; PS01046; LON SER; 1.
Hydrolase; Serine protease; ATP-binding; Complete proteome.
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ATP (POTENTIAL).
BY SIMILARITY.
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Protein At2041620.
AT2641620 OR T32G6.14.
Arabidopsis thaliana (Mouse-ear cress).
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00.0%; Pred. No. 17;
ve, 0; Mismatches
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InterPro; IPR003593; AAA ATPase.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003593; Pept S16 C.
InterPro; IPR004815; Pept S16 N.
InterPro; IPR004815; Pept S16 N.
InterPro; IPR001384; Peptidase_S16.
Pfam; PF00004; AAA; I.
Pfam; PF00360; LON; I.
Pfam; PF0382; Lon C; I.
PRINTS; PR00830; ENDOLAPTASE.
SMART; SM0382; AAA; I.
                 send an email to license@isb-sib.ch)
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                                                      EMBL; AE000050; AAB96152.1;
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Best Local Similarity 100...
Best Local 8; Conservative
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                                                                       PIR; S73830; S73830.
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                                                                                        MEROPS; S16.004;
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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OR CORRESPONDED ON CORRESPONDE ON CORRESPONDED ON CORRESPONDED ON CORRESPONDED ON CORRESPONDED
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IsoId=092985-4; Sequence=VSP 002757;
TISSUE SPECIFICITY: EXPRESED FREDOMINANTLY IN SPLEEN, THYMUS, AND
PERIPHERAL BLOOD LEUKOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 273:29210-29217(1998).

FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
STIMULATED RESPONSE ELEMENT (ISRE) IN IFN PROMOTERS AND IN THE Q
PROMOTER (QP) OF EBV NUCLEAR ANTIGEN-1 (EBNA1).

SUBCELJULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
MEDLINE=97459673; PubMed=9315633;
Zhang L., Pagano J.S.;
"IRF-7, a new interferon regulatory factor associated with Epstein-Barr virus latency.";
Mol. Cell. Biol. 17:5748-5757(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM D).
MEDLINE=99003279; PubMed=9786932;
AN W.-C., MOONEP D.A., LaFleur D.W., Tombal B., Pitha P.M.;
"Characterization of the interferon regulatory factor-7 and its
potential role in the transcription activation of interferon A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grossman A., Nicholl J., Antonio L., Luethy R., Suggs S., Sutherland G.R., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=B; Synonyms=Beta;
IsoId=092985-2; Sequence=VSP_002760;
Name=C; Synonyms=Gamma;
IsoId=092985-3; Sequence=VSP_002758; VSP_002759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4;
                                                                                                                                     TRF7 HUMAN STANDARD; PRT; 503 AA. Q92985; 0000331; 000332; 0000331; 075924; 01-N0V-1997 (Rel. 35, Created) 28-FEB-2003 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Interferon regulatory factor 7 (IRF-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the IRF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=092985-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005737; C:cytoplasm; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U73036, AAB17190.1, -. EMBL, U53830, AAB80686.1; -. EMBL, U53831, AAB80680.1; -. EMBL, U53822, AAB806590.1; -. EMBL, AF076494, AAC70999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:6122; IRF7.
MIM; 605047; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P23906; ZIRF.
TRANSFAC; T04674; -.
TRANSFAC; T05106; -.
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
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                                                               RESULT 5
IRF7 HUMAN
ID TO 01-NOV.
DT 01-NOV.
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                                                                                                                                                                                                                                                                             TRYPTOPHAN PENTAD REPEAT.
MALAPE -> MPVPERPAAGPDSPRPGTR (in isoform
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN PRESENCE OF ATP. DEGRADES THE REGULATORY PROTEINS RCSA AND SOLIA. HYDROLYZES TWO ATPS FOR EACH PEPTIDE BOND CLEAVED IN THE PROTEIN SUBSTRATE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin, casein and denaturated serum albumin, in presence of ATP.
GO; GO:0005634; C:nucleus; TAS.
GO; GO:0003704; F:specific RNA polymerase II transcription fa. . .;
GO; GO:0000125; P:negative regulation of transcription from P. . .;
GO; GO:0000515; P:negative regulation of transcription from P. . .;
GO; GO:0000515; P:negative regulation of transcription from P. . .;
GO; GO:0000515; P:negative regulation of transcription from P. . .;
FO:0000515; P:negative regulation; DNA-binding; Nuclear protein; Activator;
Transcription regulation; DNA-binding; Nuclear protein; Activator;
                                                                                                                                                                                                                                                                                                                                                              GGPPGPFLAHTHA -> AQGSLLGSCTGGQ (in
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E -> K (IN REF. 2).
Q -> R (IN REF. 3).
AA6A39E0E272727C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 /FTIGLEVSP 002758.
Missing (in isoform C).
FTIGLEVSP 002759.
Missing (in isoform B).
/FTIGLEVSP_002760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to peptidase family S16.
                                                                                                                                                                                                                                                                                                                                            /FTId=VSP_002757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
LON OR MPN332 OR MP504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           795 AA.
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Similarity 100.0%; Pred. No. 12;
8; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 PSPGPOPA 364 V
                                                                                                                                                                                                                                                                                                                                                                                                                                   503
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412 4
503 AA;
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                                                                                                                                                                                                                                                                                                                                                                  152
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=90066348; PubMed=2511421;
Shaw D.R., Richter H., Giorda R., Ohmachi T., Ennis H.L.;
Shaw D.R., Richter H., Giorda R., Ohmachi T., Ennis H.L.;
Nucleotide sequences of Dictyosellum discoideum developmentally regulated cDNAs rich in (AAC) imply proteins that contain clusters of asparagine, glutamine, or threonine.";
Mol. Gen. Genet. 218:453-459(1989).
--- DEVELOPMENTAL STAGE: The concentration of AAC-rich mRNAs is low in dormant spores and growing cells, but increases during spore-germination and multicellular development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MÎSCELÎANEOUS: Several proteins derive from AAC-rich mRNA, which, due to a frameshift also have ACA and CAA codons and thus are Asn-, Thr- or Gln-rich.
                     PRINTS; PR00448; NSFATTACHMNT.
Transport; Protein transport; Endoplasmic reticulum; Golgi stack.
SEQUENCE 292 AA; 32805 MW; C9BD75D8128E19E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 448;
                                                                                                                  Length 292;
                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D8FD80D910D99817 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                              01-07N-1990 (Rel. 13, Created)
01-07N-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                 1.0%; Scort
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC-rich mRNA clone AAC11 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                          448 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASN-RICH
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PIR, S05355; S05355.
DictyBase, DDB0001892; AAC11.
InterPro; IPR000637; AT hook.
InterPro; IPR000116; Highmoblty_IY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02178; AT_hook; 4.
PRINTS; PR00929; ATHOOK.
PRODOD; PD005593; Highmoblty_IY; 1.
SMART; SM00384; AT_hook; 4.
DNA-binding; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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25
144
Pfam; PF02071; NSF; 2
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                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           AAC2 DICDI
ID AAC2 DICDI
AC P14196;
                                                                                                                    Query Match
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DOMAIN
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Nucleic Acids Res. 3:1944-1954(2003)
-:- FUNCTION: Required for vesticular transport between the endoplasmic reticulum and the Golgi apparatus (By similarity).
-:- SUBCELLULAR LOCATION: Cytoplasmic peripheral membrane protein (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                   Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
Dythedrosis virus.";
Virology 202:586-605(1994).
-!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=74-OR23-1A / FGSC 987;
MEDLINE=22542210; PubMed=12655011;
Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 8; DB 1; Length 71; 100.0%; Pred. No. 2.1; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AA; 8569 MW; ADFF85AC68E16DD3 CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable vesicular-fusion protein sec17 homolog.
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-!- SIMILARITY: Belongs to the SNAP family.
                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                  MEDLINE=94303173; PubMed=8030224;
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InterPro; IPR008941; TPR-like.
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Hypothetical protein
SEQUENCE 71 AA;
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Matches 8; Conserv
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                       SEQUENCE FROM N.A.
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Q9P6A5;
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SC17 NEUCR RESULT 3

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NCBI TaxID=46015;
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RADAIN = C. Richards S., Ashburner M., Henderson S.N.,

RADAIN = C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.

RADAIN = C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.

RADAIN = C., RADAIN = C., Blazen C.R., Miklos G.L.G.,

RADAIN = C., Radain A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RADAIN J.F., Agbayani A., An H.-J., Andrews Pfannkorh C., Baldwin D.,

RADAIN J.F., Benos P.V., Berman B.P., Bandaru D., Bolshakov S.,

RADAIN S., Benos P.V., Bender B.D., Brottler P.,

RADAIN S., Benos P.V., Bender S., Mays A.D., Dew I., Dietz S.M.,

RADAION E., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RADAION K.J. Bangelista C.C., Ferraz C., Ferriera S., Plaischman W.,

RADAION K.J. Bangelista C.C., Ferraz C., Ferriera S., Plaischman M.,

RADAIN M., Bangelista C.C., Ferraz C., Ferriera S., Rialschman M.,

RADAIN M., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RADAIN M., Ralush F., Karpen G.H., Ke Z., Kannison J.A., Kalum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J.H., Ni M. M., Nelson D.L.,

RADAIN M., Malush T.C., McLeod M.P., Moshrefi A.,

RADAIN M., Pittman G.S., Pan S., Pollard J., Puri, V., Resee M.G.,

RADAIN M., Pittman G.S., Pan S., Pollard J., Puri, V., Resee M.G.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Sylekas R. Tector C., Turner R., Wand A.H., Wang X.,

Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

Sylekas R., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RADAIN M., Warsen D., Wang S., Yao Q., Zhen G.,

Shine B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E.,

Sylekas R., Tector C., Turner R., Veners W., Saith H.O.,

RADAIN M., March M., Wang Y., Yao Q., Zhao 
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MEDLINE=22426066; PubMed=12537569;
Stapleron M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93317591; PubMed=8327460;
Kokubo T., Gong D.-W., Roeder R.G., Horikoshi M., Nakatani Y.;
"The Drosophila 110-kba transcription factor TFIID subunit directly
interacts with the N-terminal region of the 230-kba subunit.";
Proc. Natl. Acad. Sci. U.S.A. 90:5896-5900(1993).
                                                                                                                SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF 519-540; 597-616
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF 398-406; 520-540
                                                                                                                                                                                                                                                 "Molecular cloning and functional analysis of Drosophila TAF110 reveal properties expected of coactivators."; Cell 72:247-260(1993).
                                                                                                                                                                                   MEDLINE=93145526; PubMed=7678780;
Hoey T., Weinzierl R.O.J., Gill G., Chen J.-L., Dynlacht B.D.,
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
-!- FUNCTION: TFIID is a multimeric protein complex that plays a central role in mediating promoter responses to various activators and repressors. May function as a coactivator by serving as a site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005669; C:transcription factor TFIID complex; IPI.
GO; GO:0016251; F:general RNA polymerase II transcription fac. . .; IE
GO; GO:0006352; P:regulation of transcription, DNA-dependent; IPI.
InterPro; IPR007900; TAF4.
InterPro; IPR003894; TAF hom.
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                                                                                                              of protein-protein contact between activators like Spl (or btd) and TFILD complex.
SUBUNIT: TFILD is composed of TATA binding protein (TBP) and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulation; Nuclear protein; Alternative splicing 33 383
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 8.6 kDa protein in IAPI-SOD intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 921;
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/FIId=VSP 004441.
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-> M (IN REF. 4).
27E6852859872767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P47825-2; Sequence=VSP_004441;
Note=No experimental confirmation available;
-!-SIMILARITY: BELONGS TO THE TAF2C FAMILY.
-!-SIMILARITY: Contains 1 TAFH/NHR1 domain.
                                                                                                                                                                                                                                                                                                     Event=Alternative splicing, Named isoforms=2;
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1.1%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          IsoId=P47825-1; Sequence=Displayed;
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POLY-GLN.
POLY-GLN.
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EMBL; 86350; AARST433.1; -.
EMBL; AE003528; AAF49536.1; -.
EMBL; AY069807; AAL39952.1; -.
                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Nuclear. ALTERNATIVE PRODUCTS:
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SMART; SM00549; TAFH; 1.
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TRANSFAC; T02121; -.
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AC P41433;
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T2D3 DROME
T2D3 DROME
STANDARD; PRT; 921 AA.
AC P47825; P49845; Q8T9E0; Q9VUY7;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 34, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Transcription initiation factor TFIID 110 kDa subunit (P110)
GN TAF4 OR TARI10 OR CG5444.
OS Drosophila melanogaster (Fruit fly).
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UREL HELMU

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PSE2 RAT

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LICH VIBCH

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TPM3 TRICO

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OVJ3 HUMAN

OVJ3 HUMAN

PTPA RREC

LIETT SABIT

RAPR DLCDI

G3P2 AGRBI

G3P2 AGRBI

G3P2 AGRBI

G3P2 AGRBI

G3P2 AGRBI

PHEM COLLI

YHFX ECOLI

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203 SELAAAEA 210 |||||||| 756 SELAAAEA 763

9 P

Search completed: October 1, 2004, 07:33:26 Job time : 33 secs

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A,Cross-references: CB:AE002047; GB:AE000513; NID:g6459915; PIDN:AAF11680.1; PID:g645992
A,Experimental source: strain R1
A,Genet:DR2130
A,Map position: 1
A;Reference number: A75250; MUID:20036896; PMID:10567266
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100.0%; Pred. No. 60;
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Best Local Similarity
                                    A, Accession: C75313
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-840 < WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypochetical protein At2941620 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein T32G6.14
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Aseason: T00818; A84844
Richary, November 1999
Aiscession: T00818
Aiscession: Molecule Fype: DN
Aiscession: A
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No. Introna: 43/3; 74/2; 96/3; 116/3; 134/3; 234/3; 266/3; 311/3; 329/3; 368/3; 669/3; 725
A,Note: TJ2G6.14
C,Superfamily: Arabidopsis thaliana hypothetical protein At2g41620
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C.; Ma
                                    A Gene: lon, FlO orf795
A Geneic code. SGC3
C, Superfamily: ATP-dependent Lon protease
C, Keywords: ATP, TP-dependent Lon protease
C, Keywords: ATP, DNA binding, heat shock; hydrolase; nucleotide binding; P-loop; serine
F, 379-386/Region: nucleotide-binding motif A (P-loop)
F, 442-447/Region: nucleotide-binding motif B
F, 702/Active site: Ser #status predicted
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C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: C75313
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R., M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
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1.0%; Score 8; DB 1;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches
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helicase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Accession: A64714
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Feterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Tile: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID: 97394467; PMID: 9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE000653; GB: AE000511; NID: 92314733; PIDN: AAD08593.1; PID: 9231472
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Uul-1998 #text_change 20-Jun-2000
C;Accession: B70748
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Perkhill, M.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:9829597; PMID:9634230
A;Reference number: A70500; MUID:9829597; PMID:9634230
A;Accession: B70748
A;Accession: B70748
A;Molequle type: DNA
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A;Cross-references: GB:Z74697; GB:AL123456; NID:g3261602; PIDN:CAA98982.1; PID:g1405958
A;Experimental source: strain H37Rv
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    Length 840;
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Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches
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C;Superfamily: chromosome segregation protein SMC1
1.0%; Score 8; DB 2;
100.0%; Pred. No. 41;
                                           Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                A;Cross-references: GB:AE004219; GB:AE003852; NID:g9655899; PIDN:AAF94566.1; GSPDB:GN0012
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
C;Genetics:
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N;Alternate names: ATP-dependent proteinase lon; ATP-dependent serine proteinase La; hypo
N;Contains: adenosinetriphosphatase (EC 3.6.1.3)
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C;Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phosphot:
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Airtle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae. A; Reference number: S73327; MUID:97105885; PMID:8948633
A; Accession: S73830
A; Status: nucleic acid sequence not shown; translation not shown
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C;Comment: This enzyme catalyzes the hydrolysis of large proteins in the presence of ATP
                          A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A,Reference number: A82035, MUID:20406833, PMID:10952301
A,Accession: F82203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 «XUR»
A;Cross-references: GB:BA000018; PID:g13701521; PIDN:BAB42815.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ptaA [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: B89957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mycoplasma pneumoniae
A;Varitety: ATCC 29342
C;Date: 09-Apr.1999 #sequence_revision 09-Apr.1999 #text_change 02-Jun-2003
C;Accession: S73830
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 8; DB 2.
Best Local Similarity 100.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 SELAAAEA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 SELAAAEA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 8; Conservat
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   Nature 406, 477-483, 2000
                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-484 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                            A; Gene: VC1409
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A;Cross-references: EMBL:Z82086; PIDN:CAB04996.1; GSPDB:GN00023; CESP:ZK228.4
                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ZK228.4 - Caenorhabditis elegans
C;Species: caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T27791
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A;Residues: 1-448 <SHA>
A;Cross-references: EMBL:X16522; NID:97173; PIDN:CAA34529.1; PID:97174
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A;Introns: 38/1; 99/1; 143/3; 181/3; 250/2
C;Superfamily: Caenorhabditis elegans hypothetical protein F31F7.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 294;
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                                 Length 292;
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                                                                                                 0; Indels
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R;Basham, V
R;Basham, V
R;Reference to the EMBL Data Library, November 1996
A;Reference number: Z20419
A;Accession: T27791
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches
                                     DB 2;
                              1.0%; Score 8; DB 2;
100.0%; Pred. No. 16;
ive 0; Mismatches
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Query Match
Best Local Similarity 100...
Best Local 8; Conservative
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                                                                                                                                                           150 NDGAVALA 157
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q 8

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0; Indels

Length 284;

5;

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tropomyosin isoform TMII - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-Apr-1996 #sequence-revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: SS8922; S62128; SF8918
R;Kagawa, H.; Sugimoto, K.; Matsumoto, H.; Inoue, T.; Imadzu, H.; Takuwa, K.; Sakube, Y.J. Mol. Biol. 251, 603-613, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Genome structure, mapping and expression of the tropomyosin gene tmy-1 of Caeno
A,Reference number: S58918; MUID:95395840; PMID:7666414
A,Accession: S58922
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A;Reference number: Z25022
A;Accession: T49361
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A;Molecule type: DNA
A;Residues: 1-284 <kMv>
A;Cross-references: EMBL:D38539; NID:g871835; PIDN:BAA07541.1; PID:g1208410
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
A;Accession: S58918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-284 «KAG>
A;Cross-references: BMBL:D38541; NID:g871837; PIDN:BAA07544.1; PID:g1208414
A;Accession: S62128
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C;Accession: T49361
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A;Molecule type: DNA
A;Residues: 1-292 <SCH>
A;CRSidues: 1-292 <SCH>
A;Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.150
A;Experimental source: BAC clone B1D1; strain OR74A
                                            A;Gene: tmy-1
A;Introns: 15/3; 61/3; 80/3; 125/2; 164/3; 188/2; 234/3; 258/1
C;Superfamily: tropomyosin
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 15/3; 61/3; 80/3; 125/2; 164/3; 188/2; 234/3; 258/1
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                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches
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C, Keywords: alternative splicing
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A,Residues: 11-49;171-211 <KAF>
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A;Introns: 11/3; 53/1; 155/2
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                                                                                                                                                                                                                                                                                                                                                727 VEAQLKEA 734
                                                                                                                                                                                                                                                                                                                                                                                                             144 VEAQLKEA 151
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             C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: S2821; S62127; S58918
K;Kagawa, H; Sugimoto, K.; Matsumoto, H.; Inoue, T.; Imadzu, H.; Takuwa, K.; Sakube, Y.
J. Mol. Biol. 251, 603-613, 1995
A;Tile: Genome Structure, mapping and expression of the tropomyosin gene tmy-1 of Caeno
A;Reference number: S58918; MUID:95395840; PMID:7666414
A;Rolecule type: mRNA
A;Residues: 1-284 <KAG>
A;Cross-references: EMBL:D38540; NID:g1208412; PIDN:BAA07543.1; PID:g1208413
A;Accession: S62127
A;Rolecule type: DNA
A;Residues: 1-276, VNIP', 280-284 <KAF>
A;Cross-references: EMBL:D38539; NID:g871835; PIDN:BAA07540.1; PID:g1208409
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
A;Residues: 11-76, VNIP', 280-284
A;Residues: 11-76, VNIP', 280-284
A;Residues: 11-49;171-211 <KRW>
Cell 72, 247-260, 1993

A; Title: Molecular cloning and functional analysis of Drosophila TAFIIO reveal propertie A; Fafetenece number: A45183; MUID: 93145326; PMID: 7678780

A; Reference number: A45183

A; Status: preliminary; not compared with conceptual translation

A; Residues: 1-921 and being a caid

A; Construction

A; Cross-references: FlyBase: FBgn0010280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACOTÉ-29 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dSDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: E72853
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUD:94303173; PMID:8030224
A;Reference number: A72853
A;Accession: E72833
A;Accession: E72833
A;Residues: 1-71 <AXR>
A;Residues: 1-71 <AXR>
A;Residues: 1-71 <AXR>
A;Gross-references: GB:L22858; NID:g510708; PIDN:AAA66659.1; PID:g559098
C;Genetics:
A;Gene: Acorf-29
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100.0%; Pred. No. 4.4
iive 0; Mismatches
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100.0%; Pred. No. 4.3
tive 0; Mismatches
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Best Local Similarity 100.0
Matches 9; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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hypothetical protein phtE-truncation [imported] - Streptococcus pneumoniae (strain R6) (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (C)Species: Streptococcus pneumoniae (C)Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 (SAccession: F97985 (SAccession: F97985 (C)Accession: F97985 (C)Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Kokubo, T.; Gong, D.W.; Roeder, R.G.; Horikoshi, M.; Nakatani, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, S896-5900, 1993
A,Title: The Drosophila 110-kDa transcription factor TFIID subunit directly interacts
A,Reference number: A48184; MUID:93317591; PMID:8327460
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A;Cross-references: GB:AE007317; PIDN:AAK99714.1; PID:g15458517; GSPDB:GN00174
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C,Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
C,Accession: A45183
R,Hoey, T.; Weinzierl, R.O.; Gill, G.; Chen, J.L.; Dynlacht, B.D.; Tjian, R.
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C,Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999
C,Accession: A48184
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A;Experimental source: embryo nuclear extract
A;Note: sequence extracted from NCBI backbone (NCBIN:134863, NCBIP:134864)
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A45183
TBP-associated factor TFIID - fruit fly (Drosophila sp.)
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Pred. No.
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100.0%; Pred. No.
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A,Cross-references: FlyBase:FBgn0010280
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                                                                      92 YNGKVPYDAIISEELLM 108
              85
              69 YNGKVPYDAIISEELLM
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A,Status: preliminary
A,Molecule type: mRNA, protein
A,Residues: 1-921 «KOK»
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Matches 10; Conservative
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95115
A;Accession: H95115
A;Accession: Preliminary
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-1039 «KUR»
A;Accession: GB:AE005672; PIDN:AAK75121.1; PID:g14972477; GSPDB:GN00164; TIGR:SP4
C;Genetics:
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R;Spellerberg, B.; Roadzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luer Infect. Immun. 67, 871-878, 1998
A;Title: Lmb., a protein with similarities to the LraI adhesin family, mediates attachmen A;Reference number: 224091; MUID:99115568; PMID:9916102
A;Accession: T4658
A;Accession
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. B. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A;Reference number: A97872; MUD:21429245; PMID:11544234
A;Accession: D97985
A;Accession: D97985
A;Molecule type: DNA
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A)Cross-references: EMBL:AF062533; NID:g4249622; PIDN:AAD13797.1; PID:g4249624
A)Experimental source: strain R268
C)Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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C.Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
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;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000
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2.3e-23;
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4.0%; Score 32; DB 2; Lo
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0;
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A.Reference number: A95000; MUD:21357209; PMID:11463916
A.Rocession: G95115
A.Rocession: G95115
A.Residue: preliminary
A.Molecule type: DNA
A.Residues: 1-839 cKUR>
A.Residues: 1-839 cKUR>
A.Streptococcus gnamental source: strain TIGR4
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Cispecies: Streptococcus pneumoniae
Cibate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
Cibate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
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                                                                                                                                                                                      C;Accession: G95115
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heion, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt.
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A;Status: preliminary
A;Nolecule type: DNA
A;Rosidues: 1.853 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99711.1; PID:g15458514; GSPDB:GN00174
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                                                - Streptococcus pneumoniae
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                                                                                           C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
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C;Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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Best Local Similarity 100.0%; Pred. No. 7.6e-52;
Matches 60; Conservative 0; Mismatches 0; Indels
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larity 100.0%; Pred. No. 7.5e-52;
Conservative 0; Mismatches 0;
                                          conserved hypothetical protein SP1003 [imported]
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C;Species: Streptococcus pneumoniae
R;Tettelin, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 299, 496-506, 2001
A;Reterince 299, 496-506, 2001
A;Reterince 299, 496-506, 2001
A;Reterince Dumber: A95000; MUID:21357209; PMID:11463916
A;Reterince number: A95000; MUID:21357209; PMID:11463916
A;Re
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D98004
histidine Motif-Containing protein [imported] - Streptococcus pneumoniae (strain R6)
C; Species: Streptococcus pneumoniae
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C; Accession: D98004
R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHofff, B.S.; E. R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M. Y. P.; Sun, P.M.; Winkler, M. E.
J. Bacteriol. 183, 5709-5717, 2001
A; Attile: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MuID:21429245; PMID:11844234
A; Status: preliminary
A; Molecule type: DNA
A; Residues: L955 < RURS
A; Rederence of the Bacterium Streptococcus pneumoniae Strain R6.
A; Status: preliminary
A; Molecule type: DNA
A; Residues: L955 < RURS
A; Rederence of the Bacterium Streptococcus pneumoniae Strain R6.
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: L955 < RURS
A; Rederence of the Bacterium Streptococcus pneumoniae Strain R6.
A; Rederence of the Bacterium Streptococcus pneumoniae Strain R6.
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: L955 < RURS
A; Rederence of Rede
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KVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNRSSVSKEKIN 796
                                                     ENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNY
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llarity 100.0%; Pred. No. 7.3e-52;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.7e-99;
Matches 107; Conservative 0; Mismatches 0;
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A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Residues: 1-828 <KUR>
A; Residues: 1-828 <KUR
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A,Gene: phtA
C,Superfamily: Streptococcus agalactiae hypothetical 92.4K protein
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Hinson, T.; Hickey, E.K.; Holt, I.E. Science 293, 499-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A. A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneum A; Reference number: A95000; MUID:21357209; PMID:11463916
A; Accession: C95136
A; Accession: C95136
A; Residues: L-802 «KUR»
A; Residues: 1-802 «KUR»
A; Residues: 1-802 «KUR»
A; Residues: Strain TiGR4
C; Genetics: Strain TiGR4
C; Genetics: Strain TiGR4
C; Genetics: Strain Streptococcus agalactiae hypothetical 92.4K protein
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796
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

C95136
Conserved domain protein SP1175 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001
C;Accession: C9136
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic

hypothetical prote endo-beta-N-acetyl probable smc prote

polyprotein -polyprotein -

S55073 S55072

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prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia;
            otitis media; pneumonia; immunisation; bactericidal
                                                                                                                                                  (BIOC-) BIOCHEM PHARMA INC.
                                  Streptococcus pneumoniae
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                                                       WO200039299-A2
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                                                                                        AAB12763 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Conservative
                                                                                                                                                                                                                                 Streptococcus pneumoniae
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antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, others madia, bacteraemia and/or pneumonia. The present sequence represents a S. pneumoniae BVH-11-2
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      meningitis,
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100.0%; Pred. No. 2e-48;
ive 0; Mismatches 0; Indels
      vaccinating against
                                                                                                                                                                                                                                                                                                                                                                                                                                     from the present invention
Streptococcal antigens useful for vaccir
otis media, bacteremia and/or pneumonia
                                                                                                    Disclosure, Fig 12, 106pp, English.
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        protein antigen,
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Charland

Rioux C,

Martin D,

Pineau I,

Brodeur BR,

99WO-CA001218. 98US-0113800P 0

completed: October 1, 2004, 07:32:24

Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine;

Streptococcus pneumoniae strain WU2 BVH-11-2 protein antigen.

(first entry)

21-NOV-2000

AAB12758;

AAB12758 standard; protein; 816 AA.

RESULT 25

AAB12758

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antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents a S. pneumoniae BVH-11 protein antigen, from the present invention
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                                       The present invention describes nucleic acids (1) encoding protein
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100.0%; Pred. No. 2e-48;
ive 0; Mismatches 0; Indels
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  Disclosure; Fig 12; 106pp; English.
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represented in the printed specification, but is based on sequence information supplied by the European Patent Office
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100.0%; Pred. No. 10. 10. 10. 10. 10. 10. 10. Mismatches
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AAB12765 standard; protein; 807 AA.
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Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
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                                                                                                                        21-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group B Streptococcus such as Streptococcus prophylactic or group as Streptococcus such as Streptococcus prophylactic or Group Streptococcus such as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or
                                                                                                                                                                                                                                                                                                     70
           The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11
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                                                                                                                                                                                                                                                                                                   TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
                                                                                                                                                                                                                                                                 Gaps
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3. le-67; 0; Indels
                                                                                                                                                                                                                                Length 840
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                                                                                                                                                                                                                              10.1%; Score 80; DB 100.0%; Pred. No. 1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae BVH-11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU75933 standard; protein; 840 AA
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                                                                                                                                                                                                                                                                                                                                                                            GKVPYDAIISEELLMKDPNY
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Best Local Similarity 100.
***rhes 80; Conservative
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                                                                                                                                                                                              Sequence 840 AA;
                                                                                                                                                            protein antigen
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The invention relates to a novel isolated polypeptide of Streptococcus pneumoniae. A polypeptide of the invention has antibacterial, antinflammatory, and auditory activity, and is used as a vaccine. The polypeptide or pharmaceutical composition is useful for the prophylactic or therapeutic treatment of streptococcal infection, meningitis, othiss media, bacteraemia or pneumonia infection. The kit is useful for detecting or diagnosing streptococcal infection. The pharmaceutical composition is useful as a vaccine. The polynucleotides are useful in designing DNA probes for detecting circulating Streptococcus in a biological sample. The present sequence is used in the exemplification of the invention. Note: The sequence data for this patent is not fully
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          polymucleocide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcul infections. This is the amino acid sequence of Streptococcus pneumoniae protein BVH-II, used to create the antigenic peptides described in the method of the invention
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Staphylococcus aureus) in an individual susceptible to the infection. A
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100.0%; Pred. No. 1e-67;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM18797 standard; protein; 840 AA
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Best Local Similarity
                                                                                                                                                                                                                         Sequence 840 AA;
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Labbe S;
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric Sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of melingitis, otitis media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcus lacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus group B Streptococcus such as Streptococcus group B Streptococcus ancreus) in an individual susceptible to the infection. A polypulocetic (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypupetides are useful in a diagnostic test for S pneumoniae infection. (III) is useful for designing DNA creat for S pneumoniae infection. (III) is useful for designing DNA sample suspected of containing the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S pneumonia nucleic acid in a sample for diagnosing streptococcus insertions. This sequence repersents a truncate of a streptococcus insertions. This sequence represents a truncate of a streptococcus insertions. This sequence represents a truncate of a streptococcus insertions. This sequence repersents a truncate of a streptococcus insertions. This sequence is a prepared to the subsection of a streptococcus insertions. The sequence repersents a truncate of the streptococcus insertions. This is sequence is the sequence of 
    useful as vaccine components for treating or preventing infections such as otitis media, meningitis, and
                                                                                                                                                                   Example 1; Page; 113pp; English
    polypeptides,
streptococcal
                                                                                 bacteremia
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Sequence 821 AA;

of a Streptococcus pneumoniae gene used to obtain antigenic peptides, described in the method of the invention. Note: This sequence does not appear in the specification but has been created according to information given in the invention

ö 70 71 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN .,0 , DB 5; Lens 0. 1e-67; 0; Indels Length 821; 10.1%; Scor. 100.0%; Pred. No. 10. ''' 0; Mismatches 71 GKVPYDAIISEELLMKDPNY 90 Conservative Query Match Best Local Similarity Matches 80; Conserv à ò

ABM18807 standard; protein; 821 AA ABM18807; RESULT 15 ABM18807 FINANCE CONTRACTOR CON

(first entry) 13-0CT-2003

S. pneumoniae variant protein BVH-11M.

antibacterial; antiinflammatory; auditory; vaccine; meningitis; streptococcal infection; otitis media; bacteraemia; pneumonia; BVH-3; mutant; mutein; New 43; BVH-11; BVH-11-2.

Streptococcus pneumoniae Synthetic

WO2003054007-A2.

03-JUL-2003

20-DEC-2002; 2002WO-CA002006.

20-DEC-2001; 2001US-0341252P

(SHIR-) SHIRE BIOCHEM INC.

Blais N, Ouellet C; Charland N, Brodeur BR, Martin D, Hamel J, Labbe S;

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                                                                                                                                                                                                      The invention relates to a novel isolated polypeptide of Streptococcus pneumoniae. A polypeptide of the invention has antibacterial, antiinflammatory, and auditory activity, and is used as a vaccine. The polypeptide or pharmaceutical composition is useful for the prophylactic or therapeutic treatment of streptococcal infection, meningitis, otitis media, bacteraemia or pneumonia infection. The kit is useful for detecting or diagnosing streptococcal infection. The pharmaceutical composition is useful as a vaccine. The polynuclectides are useful in designing DNA probes for detecting circulating Streptococcus in a biological sample. The present sequence is used in the exemplification of the invention. Note: The sequence data for this patent is not fully represented in the printed specification, but is based on sequence information supplied by the European Patent Office
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                                                                                           diagnosing, preventing or treating streptococcal infection, meningitis,
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                                                                     useful for
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                                                                                                                 otitis media, bacteremia or pneumonia infection.
                                                                     New isolated polypeptides of Streptococcus
                                                                                                                                                                 Example 1; SEQ ID NO 19; 79pp; English.
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                      WPI; 2003-569224/53.
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Best Local Similarity
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AAB12716 standard; protein; 840 AA. 21-NOV-2000 (first entry) AAB12716; 

RESULT 16 AAB12716

Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal. Streptococcus pneumoniae BVH-11 protein antigen SEQ ID NO:4.

Streptococcus pneumoniae

WO200039299-A2.

06-JUL-2000.

99WO-CA001218, 20-DEC-1999;

BIOC- > BIOCHEM PHARMA INC.

Charland Rioux C, Martin D, Pineau I, Hamel J, Brodeur BR,

WPI; 2000-452397/39. N-PSDB; AAA65731 Streptococcal antigens useful for vaccinating against e.g. meningitis, otis media, bacteremia and/or pneumonia.

Claim 18; Fig 4; 106pp; English.

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New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing
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                                                                                                                                                                                                                                                                                          The present invention describes nucleic acids (I) encoding protein antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11M
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                                                                                                                                                                                                           Streptococcal antigens useful for vaccinating against e.g. meningitis,
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                                                                                                                                      Rioux C,
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Pred. No. 1e-67;
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100.0%; Pred. No. 10.10.0%; Pred. No. 10.10.0%; Mismatches
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                                                                                                                                        Pineau I,
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                                                                                                                                                                                                                                                                  Claim 18; Fig 25; 106pp; English
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                                   99WO-CA001218.
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                                                                                                       (BIOC-) BIOCHEM PHARMA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Conservative
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                                                                                                                                          Brodeur BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouellet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-122272/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 821 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200198334-A2
                                 20-DEC-1999;
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06-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                          Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU84026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, ottiss media, bacteraemia and/or pneumonia. The present sequence represents a S. pneumoniae BWH-11 protein antigen, from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcal antigens useful for vaccinating against e.g. meningitis, otis media, bacteremia and/or pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                 Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes nucleic acids (I) encoding protein
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                                                                                                                                                                                                                                                                                                                                                                           Charland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae BVH-11M protein antigen SEQ ID NO:60.
                                                     Streptococcus pneumoniae strain SP64 BVH-11 protein antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%; Score 80; DB 3; Length 821; 100.0%; Pred. No. 1e-67; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                           Rioux C,
                                                                                                                                                                                                                                                                                                                                                                             Martin D,
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                                                                                                                                                                                                                                                                                                                                                                             Pinean
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                                                                                                                                                                                                                                                                                                                                          (BIOC-) BIOCHEM PHARMA INC
                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
Les 80, Conservative
                                                                                                                                                                Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                             Brodeur BR,
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                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-452397/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 821 AA;
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                      21-NOV-2000
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RESULT 11

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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or BVH-11, or chimeric sequences derived from them. A vaccine (II) comparising (I) is useful for therapeutic or prophylactic treatment of maintail susceptible to these disorders. (II) is also useful for individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus proup A streptococcus such as Streptococcus such as Streptococcus prophylactic treatment of any streptococcus such as Streptococcus aureus) in an individual susceptible to the infection. A streptococcus aureus) in an individual susceptible to the infection. A colymuleotide (III) encoding (I) is useful in DNA immunisation techniques. The Streptococcus polypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA creptococcus infections of III) is useful in a sample for sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for described in the method of the invention. Note: This sequence does not appear in the specification but has been created according to information arithe according to information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and
                                                                                                                                                                         BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brodeur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Le...
                                                                                                                                     Truncated variant of S. pneumoniae BVH-11, NEW16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 80; DB 100.0%; Pred. No. 8.8 ive 0; Mismatches
                       AAU84093 standard; peptide; 690 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charland N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 GKVPYDAIISEELLMKDPNY
                                                                                                                                                                                                                                                                                                                                                19-JUN-2001; 2001WO-CA000908.
                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-2000; 2000US-0212683P
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Conservative
                                                                                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              given in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouellet C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-122272/16
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Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 690 AA;
                                                                                                                                                                                                                                                                      WO200198334-A2.
                                                                                                 08-MAY-2002
                                                             AAU84093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamel J,
AAU84093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel isolated polypeptide of Streptococcus pneumoniae. A polypeptide of the invention has antibacterial, antiintlammatory, and auditory activity, and is used as a vaccine. The polypeptide or pharmaceutical composition is useful for the prophylactic or therapeutic treatment of streptococcal infection, meningitis, otitis media, bacteraemia or pneumonia infection. The kit is useful for detecting or diagnosing streptococcal infection. The pharmaceutical composition is useful as a vaccine. The polymucleotides are useful in designing DNA probes for detecting circulating streptococcus in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polypeptides of Streptococcus pneumoniae, useful for diagnosing, preventing or treating streptococcal infection, meningitis, otitis media, bacteremia or pneumonia infection.
                                                                                                                                             antibacterial; antiinflammatory; auditory; vaccine; meningitis; streptococcal infection; otitis media; bacteraemia; pneumonia; BVH-3; mutant; mutein; New 43; BVH-11; BVH-11-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouellet C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Blais N,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 38; 79pp; English.

 S. pneumoniae variant protein NEW16.

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             ABM18826 standard; protein; 690 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 GKVPYDAIISEELLMKDPNY 91
                                                                                                                                                                                                                                                                                                                                  20-DEC-2002; 2002WO-CA002006.
                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2001; 2001US-0341252P
                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                   Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-569224/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                WO2003054007-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 690 AA;
                                                                                13-OCT-2003
                                                                                                                                                                                                                                                                                                 03-JUL-2003.
                                                                                                                                                                                                                               Synthetic.
                                                ABM18826;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamel J,
Labbe S;
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ABM18826
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Length 334;

Score 80; DB 7;

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described in the method of the invention. Note: This sequence does not appear in the specification but has been created according to information given in the invention
                                                                                                                                                                          11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70
                                                                                                                                                                                              12 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYYYN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polypeptides of Streptococcus pneumoniae, useful for diagnosing, preventing or treating streptococcal infection, meningitis, otitis media, bacteremia or pneumonia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial; antiinflammatory; auditory; vaccine; meningitis; streptococcal infection; otitis media; bacteraemia; pneumonia; BVH-3; mutant; mutein; New 43; BVH-11; BVH-11-2.
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouellet C;
                                                                                                                                          ;
0
                                                                                                        Length 334;
                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blais N,
                                                                                                                        4.5e-68;
hes 0;
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                                                                                                          DB 5;
                                                                                                        10.1%; Score 80; DB 100.0%; Pred. No. 4.5 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 20; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. pneumoniae variant protein BVH-11A.
                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                               71 GKVPYDAIISEELLMKDPNY 90
                                                                                                                                                                                                                                                                            72 GKVPYDAIISEELLMKDPNY 91
                                                                                                                                                                                                                                                                                                                                                                    ABM18808 standard; protein; 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-2002; 2002WO-CA002006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2001; 2001US-0341252P
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charland N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-569224/53
                                                                                                                          Best Local Similarity
                                                                         Sequence 334 AA;
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                                                                                                                                          80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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Labbe S;
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                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                     ABM18808
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Sequence 334 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN 70
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                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcal antigens useful for vaccinating against e.g. meningitis, otis media, bacteremia and/or pneumonia.
                                                                            11 TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charland N;
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                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae NEW16 protein antigen SEQ ID NO:79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1%; Score 80; DB 3; L
100.0%; Pred. No. 8.8e-68;
ive 0; Mismatches 0;
            4.5e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D,
                            Mismatches
               Pred. No.
                                                                                                                                                                                                                               AAB12745 standard; protein; 690 AA.
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10.001
100.001
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                                                                                                                      71 GKVPYDAIISEELLMKDPNY
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                                                                                                                                                                                                                                                                                        (first entry)
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Matches 80; Conservative
                              80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamel J, Brodeur BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-452397/39.
Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 690 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein antigen
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TVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYN

10.1%; Score 80; DB 3; Length 334; 100.0%; Pred. No. 4.5e-68; ive 0; Mismatches 0; Indels

Conservative

Similarity 80; Conserv

Best Loca Matches

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Sequence 334 AA; protein antigen

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Query Match Local

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               EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 620
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                                                                                        EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY 600
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                                                                                                                                                                                                      LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP 740
                                                                                                                                                                                                                            QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMABAEKLLA 780
                                                                                                                                                                                                                                           VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
                                                                                                                                                      621 NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLED
                                                                                                                                                                                LPATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP
                                            KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                                                                                                                                    NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAMFDDHTYKAPNGYTLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcal antigens useful for vaccinating against e.g. meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charland N;
                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae BVH-11A protein antigen SEQ ID NO:61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           otis media, bacteremia and/or pneumonia.
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                                                                                                                                                                                                                                                                                         LLKGSNPSSVSKEKIN 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae
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The invention describes an isolated polypeptide (1) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or the BVH-11, or chimeric sequences derived from them. A vaccine (II) or chimeric sequences derived from them. A vaccine (III) or chimeric sequences derived from them. A vaccine (III) comprising (I) is useful for therapeutic or prophylactic treatment of prophylactic treatment of any streptococcal bacterial or therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus promoniae, group A streptococcus such as Streptococcus pyogenes, group B Streptococcus such as Streptococcus pyogenes, group B Streptococcus avacus) in an individual susceptible to the infection. A polymucleotide (III) encoding (I) is useful in DNA immunisation termiques. The Streptococcus pypeptides are useful in a diagnostic test for S. pneumoniae infection. (III) is useful for designing DNA probes may also be constaining the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus in a biological cused for detecting enemonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence represents a truncate of a Streptococcus pneumoniae gene used to obtain antigenic peptides,
                                                                                                                                                                                                               BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia; streptococcal bacterial infection; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brodeur
                                                                                                                                                                      Truncated variant of S. pneumoniae BVH-11, BVH-11A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charland N, Martin D,
                                         AAU84027 standard; peptide; 334 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2001; 2001WO-CA000908
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                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                    AAU84027;
RESULT 7
                      AAU84027
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The present invention describes nucleic acids (1) encoding protein antigens (11) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence represents the S. pneumoniae BVH-11A

Claim 18; Fig 26; 106pp; English.

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            KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                                                                                                                                                          EGDAYUTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                   ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPG
                                                                       POPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
                                                                                                          VSHTLTAKKENVAPRDQEFYDKAYNLLTBAHKALFXNKGRNSDFQALDKLLERLNDESTN
                                                                                                                        VSHTLTARKENVAPRDQBFYDKAYNLLTBAHKALFENKGRNSDFQALDKLERLNDESTN
                                                                                                                                                                                  EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
                                                                                                                                                                                                                      NRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              histidine triad residue; Sp36; antibody; otitis media;
nasopharymgeal infection; bronchial infection; bronchitis; sepsis;
meningitis; lobar pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae; infection; vaccine; coiled coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant variant of Sp36 (Sp36A) of S. pneumoniae.
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/label= Coiled coil region
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Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHH) or a colled-coil region, or an antibody directed against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumococcal infections which includes otitis media, nasopharyngeal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHADNVRIKEEINRQKQEHSQHREGGIPRNDGAVALARSQGRYITDDGYIFNASDIIEDT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AHADNYKTKEEINKOKOEHSOHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
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larity 99.9%; Pred. No. 0;
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/label= Histidine triad res
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/label= Coiled coil region
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Tettelin H,

Masignani V,

WPI; 2003-040579/03.

N-PSDB; ABX06886

CHIRON SPA. INST GENOMIC RES

27-MAR-2002; 2002WO-IB002163 27-MAR-2001; 2001GB-00007658

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                                                     AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                            AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                                                         GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
                                                                                                                                                              VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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S. pneumoniae type 4 strain protein from coding region #1174. Ŕ ABU01598 standard; protein; 802 (revised)
(first entry) 23-OCT-2003 11-FEB-2003 ABU01598; 

sepsis; otitis media; ear infection; immunostimulant; auditory; respiratory; Streptococcus pneumoniae; type 4 strain Bacterial meningitis; pneumonia; antiinflammatory; antibacterial; gene therapy; vaccine

WO200277021-A2

03-OCT-2002

246

The invention relates to a protein comprising or having at least 50% identify to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified bNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target contained within a Streptococcus nucleic acid sequence to the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes concoling the proteins has been rendered inactive. The proteins, and disease or infection due to streptococcus card molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus. Concounting a disease or infection due to streptococcus card antibiotics. The present sequence is one of the 2469 proteins expressed by the identified odding regions from the genomic sequence. Note: The sequence data for this patent did not form the genomic sequence. Note: The sequence data for this patent did not form the genomic sequence. Note: The sequence of the sequence of the fight primer of the sequence of the fight. 120 180 186 09 99 New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media o 7 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 127 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS 1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT 121 AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT . ij 9 DB Mismatches Score 695; I Pred. No. 0; Claim 1; SEQ ID NO 2348; 56pp; English. .: 87.3%; 795; Conservative standardise OS field) Similarity Sequence 802 AA; Query Match Best Local Si Matches 795; 61 181 187 qq à g d ò ò g

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The invention relates to an isolated polymucleotide consisting of a Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding $8028) one of 113 disclosed nucleic acids encoding 113 s. pneumoniae antigens. Also included are making a recombinant vector by inserting the nucleic acid into a vector, an isolated polymucleotide consisting of at recombinant host call comprising the $8028 nucleic acid, and a recombinant host call comprising the $8028 polymucleotide. The nucleic acids are useful as DNA vaccine against Streptococcus pneumoniae infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae antigen nucleic acids are useful as probes for use in diagnostic methods for detecting S. pneumoniae appearance in the present sequence represents an S. pneumoniae antigenic protein.
                                                                                         Novel polynucleotide encoding Streptococcus pneumoniae polypeptides useful for producing vaccines for prevention or attenuation of infection
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                    661 LFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVP
                                                                     QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLA
                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; bacterial infection; vaccine; pneumonia; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae antigenic protein SP036.
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                                                                                                                                              LLKGSNPSSVSKEKIN 796
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97US-00961083
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N-PSDB; ADC45136.
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                                                                                                                                                                                                                                      ABQ84792 to ABQ84904 represents nucleic acids which encode the prevences pneumoniae antigens given in ABP4557 to ABP54669. The S. pneumoniae antigens have autibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polymucleotides encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. ABQ84905 to ABQ8130 represent primers used in the cloning of S. pneumoniae ORFS (open reading frames) which are used in an example
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                        Fannon MR
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                                                                                                                New Streptococcus pneumoniae antigens, useful for detecting Strept and for preventing or attenuating disease caused by Streptococcus infection.
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ses 796; Conservative
                        Kunsch CA,
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N-PSDB; ABQ84819.
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The present sequence represents a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against streptococcus pneumonia, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific noritodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antighens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding antigenic peptide(s) from - or their epitope-containing fragments, useful therapeutic vaccines, and for diagnosis.
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                                                                               Streptococcus pneumoniae SP0036 protein.
                                                                                                                                                                                                                          /label= unknown
/note= "encoded by GNA"
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                                                 (first entry)
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                                      241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300
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                                                                               ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
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KUNSCH C A.
BARASH S C.
DILLON P J.
DOUGHERTY B.
FANNON M.R.
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US-10-387-783-1
; Sequence 1, Application US/10387783
; Publication W. US2004005331A1
; GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John B.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs
FILE REFERENCE: 465201-633
; FILE REPERENCE: 465201-633
; CURRENT APPLICATION NUMBER: US/10/387,783
; CURRENT FILING DATE: 2003-03-13
; PRIOR PAPLICATION NUMBER: 09/468,656
PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1999-12-21
; PRIOR FILING DATE: 1998-12-21
; OCTHURE: PRIOR DATE: 3.0
; SEQ ID NO: 1
; LENGURH: APPLICATION: Used in amplification of the Sp36 gene sequence.
; OTHER INFORMATION: used in amplification of the Sp36 gene sequence.
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Query Match
1.1%; Score 27; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 27; Conservative 0; Mismatches 0; Indels 1 TICITACGAGIIGGGACIGIAICAAGC 27 g δ

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Gaps 0;

Search completed: October 1, 2004, 07:13:14 Job time : 1914 secs

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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-686
CURRENT APPLICATION NUMBER: US/10/412,850
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: 09/468,656
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 3.0
Sequence 1, Application US/10412862
Publication No. US20040052781A1
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Workins Polypeptides Having Selected Structural;
TITLE OF INVENTION: Morise
TITLE OF INVENTION: Morise
FILE REFERENCE: 469201-685
CURRENT APPLICATION NUMBER: US/10/412,862
CURRENT PILING DATE: 2003-04-14
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 1
LEMBER OF SEQ ID NOS: 14
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100.0%; Pred. No. 0.0041;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100..
Local 27; Conservative
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nes 27; Conserva
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LENGTH: 36
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Matches
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| Sequence 3, Application US/10387783
| Sequence 3, Application US/10387783
| Sequence 3, Application No. US20040005331A1
| Publication No. US20040005331A1
| APPLICANT: Johnson, Leslie S.
| APPLICANT: Johnson, John E.
| TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
| TITLE OF INVENTION: Motifs
| TITLE OF INVENTION: Motifs
| FILE REFERENCE: 469201-683
| CURRENT APPLICATION NUMBER: US/10/387,783
| CURRENT FILING DATE: 2003-03-13
| PRIOR PPLICATION NUMBER: 60/113,048
| PRIOR PLING DATE: 1999-12-21
| PRIOR FILING DATE: 1998-12-21
                         Publication No. US20040001836A1
GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-686
CURRENT APPLICATION NUMBER: US/10/412,850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Reverse primer; CTHER INFORMATION: used in amplification of the Sp36 gene sequence. US-10-412-850-3
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1.3%; Score 30; DB 16; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 30; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                PRIOR APPLICATION DATE: 2003-04-14

PRIOR APPLICATION NUMBER: 09/468,656

PRIOR FILING DATE: 1999-12-21

PRIOR PLING DATE: 1999-12-21

PRIOR PLING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 3.0

SEQ ID NO 3

LENGTH: 40

TYPE: ....
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Best Local Similarity 100.0
Matches 30; Conservative
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LENGTH: 40
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RESULT 22

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RESULT 25

RESULT 23 US-10-412-862-1

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Fri Oct

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APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-685
CURRENT APPLICATION NUMBER: 09/468,656
PRIOR PILING DATE: 2003-04-14
PRIOR PLILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR PLILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 3
LENGTH: 40
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Pred. No. 0.00011;
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100.0%; Pred. No. 0.00011;
cive 0; Mismatches 0;
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                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 282:
                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/961,083
                                                                                                                                                                             FILING DATE: CURROWN:
ATTONBY AGENT INFORMATION:
NAME: BYCOKES, A. ANGERS
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB340
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10412862 Publication No. US20040052781A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 30; Conservative
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US-10-412-850-3/c
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                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Kunsch et al.

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRATE: Maryland
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Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
1113 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1165
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; L 5.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Unn-2002
CLASSIFICATION ATM.
PRIOR APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 08/961,527
APPLICATION NUMBER: US 08/961,527
APPLICATION NUMBER: US 08/961,527
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hyman, Mark J.
REGIGTRATION NUMBER: 46, 789
REFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
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1.8%; Score 44; DB
Best Local Similarity 100.0%; Pred. No. 5.6
Matches 44; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
OPERATING SYSTEM: Windows 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 355:
                                                                                               US-10-158-844-355; Sequence 355, Application US/10158844; Publication No. US20040029118A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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US-09-765-272-282/c
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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John B.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus;
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural;
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
CURRENT APPLICATION NUMBER: US/10/387,783
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 3.0
                                                                              GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                                                           1003 GCTCGTATTATTCCCCTTCGTTTCGTTCAAACCATTGGGTACCAGATTCAAG 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.2%; Score 53; DB 16; Length 2531; Best Local Similarity 100.0%; Pred. No. 1e-16; Matches 53; Conservative 0; Mismatches 0; Indels
                         0; Indels
100.0%; Pred. No. 1e-16; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TITLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: US/09/884,465A
CURRENT FILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09884465A Publication No. US20030077293A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        Sequence 11, Application US/10387783 Publication No. US20040005331A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shire Biochem, Inc.
Best Local Similarity 100. Matches 53; Conservative
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LENGTH: 2639
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US-09-884-465A-5
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; Publication No. US20040001836A1
; Publication No. US20040001836A1
; GENERAL IMPORMATION:
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Adamou, John E.
; TITLE OF INVENTION: Pneumoniae Polypeptides Having Streptococcus;
; TITLE OF INVENTION: Motified Polypeptides Having Selected Structural;
; TITLE OF INVENTION: Motified Polypeptides Having Selected Structural;
; TITLE OF INVENTION: Motified Polypeptides Having Selected Structural;
; TITLE OF INVENTION: Motified Polypeptides Having Selected Structural;
; FILE REFERENCE: 469201-686
; CURRENT APPLICATION NUMBER: 09/468,656
; CURRENT FILING DATE: 2093-04-21
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 11
ILENGTH: 2531
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Sequence 5, Application US/10387783

Sequence 5, Application US/10387783

Publication No. US20040005331A1

GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

FILE REFERENCE: 469201-683

CURRENT APPLICATION NUMBER: US/10/387,783

CURRENT FILING DATE: 2003-03-13

PRIOR FILING DATE: 1999-12-21

PRIOR FILING DATE: 1999-12-21

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver: 3.0

SEG ID NO 5

LENGTH: 2531
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1e-16;
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1e-16;
                                                                                                             2.2%; Score 53; DB
100.0%; Pred. No. 1e-
tive 0; Mismatches
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     TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                      Conservative
                                                                                                                                       Local Similarity
es 53; Conserv
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                                                           US-10-412-850-5
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PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 3.0
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SOFTWARE: Patentin Ver. 3.0
                                                                               SEQ ID NO 5
LENGTH: 2531
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TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Motifs
TITLE REPERENCE: 469201-685
CURRENT APPLICATION NUMBER: US/10/412,862
CURRENT FILING DATE: 2003-04-14
PRIOR APPLICATION NUMBER: 09/468,656
PRIOR FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1879 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1931
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100.0%; Pred. No. 1e-16;
tive 0; Mismatches 0; Indels
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                                                                       NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: P8340P1D1
INFORMATION FOR SEQ 1D NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
APPLICATION NUMBER: US 60/029,960 FILING DATE: 1996-10-31 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 206, Application US/09769787

Publication No. US20030091577A1

GENERAL INFORMATION:

APPLICANT: Microbial Technics Limited

APPLICANT: Gilbert, Christophe FG

APPLICANT: Hansbro, Philip M

TITLE OF INVENTION: Proteins

CURRENT APPLICATION WINDER: US/09/769, 787

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: GB 9816337.1

PRIOR FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-19

NUMBER OF SEQ ID NOS: 388

SOFTWARE: PATCHING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 388

SOFTWARE: PATCHING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 388

SEQ ID NO 206

LENGTH: 2481
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 243:
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Publication No. US20040052781A1
GENERAL INFORMATION
APPLICANT: Johnson, Leelie S.
APPLICANT: Adamou, John E.
                                                                                                                                                                                                                                                     STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
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RESULT 13
US-10-412-860-5
; Sequence 5, Application US/10412850
; Publication No. US20040001836A1
; GENREAL INFORMATION:
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Adamou, John E.
; TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
; TITLE OF INVENTION: Motife S.
; TITLE OF INVENTION: Waccine Compositions Comprising Streptococcus
; TITLE OF INVENTION: Worlies: 101/412,850
; TITLE OF INVENTION: MOTIFE: US/10/412,850
; CURRENT APPLICATION NUMBER: US/10/412,850
; CURRENT FILING DATE: 2003-04-14
; PRIOR FILING DATE: 1998-12-21
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SCOTWARE: PatentIn Ver. 3.0
; SEQ ID NO 5
; LENGTH: 2531
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| Sequence 11, Application US/10412862
| Publication No. US20040052781A1
| GENERAL INFORMATION:
| APPLICANT: Johnson, Leslie S. | APPLICANT: Johnson, John E. | TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus | TITLE OF INVENTION: Motifs | TITLE OF INVENTION: Motifs | TITLE OF INVENTION: Motifs | TITLE OF INVENTION | Motifs | TITLE OF INVENTION | WOHER: US/10/412,862 | CURRENT APPLICATION NUMBER: US/10/412,862 | CURRENT FILING DATE: 1999-12-21 | PRIOR FILING DATE: US/10/13,048 | PRIOR PRIOR DATE: US/10/13,048 | PRIOR DATE: US/10
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                                                                                                                                                                                                                 Query Match
2.2%; Score 53; DB 13; Length 2531;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels
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TYPE: DNA
CRGANISM: Streptococcus pneumoniae
US-10-412-862-5
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Sequence 243, Application US/10158844
Sequence 243, Application US/10158844
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 996
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                                                                                                                                                     COUNTER TRAINER PRAINER

ZIP: 20850

COMPUTER READABLE PRM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272

FILING DATE: 22-040-2001

CLASSIFICATION: CURROWN.>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2290;
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2.2%; Score 53; DB 9; Length 229
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 53; Conservative 0; Mismatches 0; Indels
                          NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410, Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
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SEQUENCE DESCRIPTION: SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/961,083
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2290 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 65:
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                                                                                                                 CITY: Rockville
STATE: Maryland
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US-10-158-844-243
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100.0%; Pred. No. 3.4e-67;
tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                         Length 2523;
                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                            Score 148; DB 10;
Pred. No. 3.3e-67;
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100.0%; Pred. No. ...
0; Mismatches
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APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Ouellet, Catherine
TILE REFERENCE: 055190-0044
CURRENT APPLICATION NUMBER: 40/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR SEQ ID NOS: 384
SOFTWARE: PATENTIN VERSION 3.1
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Patent No. US20020061615431
GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/09884465A; Publication No. US20330077293A1; GENERAL INFORMATION: APPLICANT: Shire Blochem, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                  TYPE: DNA ORGANISM: Streptococcus pneumoniae
    NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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Best Local Similarity 100.0
Matches 148; Conservative
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Best Local Similarity
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US-09-765-272-65
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IIS-09-884-465A-3
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US-09-884-465A-4
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4-4 H-H 4-4	661 TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720		CTCAAAT 401 ACCATTG 102 ACCATTG 407 STCCAGG 108	091 CCGCCAACCTGCACCAAATCTTAAATAGACTCCAAATCTTTTTTTT	126 431 132 437	AGGGTCG 1 AGGGTCG 4 CGACTAA 1 CGACTAA 4 CGACTAA 4	1 3 1 3

GAATTTGACTCCTGATGAGGTTAGCAA 120 CAAGATAACAGACCAAGGCTATGTCAC 180 TRAGGITCCTTATGACGCTATCATCAG 240 GCTAAAAGATGAGGATATTGTTAATGA 3352 0 GCTAAAAGATGAGGATATTGTTAATGA 300 GGTTAAGGAAATAATCGTGTTTCCTA Gaps 0 DB 13; Length 8195; 1; Indels **a** & a

RESULT 5
US-10-158-844-94
; Sequence 94, Application US/10158844
; Publication No. US20040029118A1
; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10387783
Fublication No. US20040005331A1
GENERAL INFORMATION
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Pneumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: MOMBER: US/10/387,783
CURRENT FILING DATE: 2003-03-13
FRIOR APPLICATION NUMBER: 09/468,656
PRIOR FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 9
LENGTH: 2451
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TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC
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                                             1 TICTTACGAGITGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA
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CCATION: (1)..(2451)

CTHER INFORMATION: n = a,

US-10-387-783-9
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ORGANISM: Streptococcus
FEATURE:
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US-10-387-783-9
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661 TICAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 720	TCAACGACATGTAGAATCTGATGGCCTTGATGCAGGCCAGAATCACAAGTCACAGTATCACAAGTCACAGTATCACAAGTCACAGTATCACAGTATGACATGATGATCACATGTAGATCACAGTAGTTGTCTTTGATCCAGCACAAATCACAAAGTAGCTAGATCATGCACACACA	CATTG	1021 GGTACCAGATTCAAGGCCAGAACAACCAACGAACCGAAC	ACGAAAAGTIGGGGAAGGAIAIGIATICGAAGAAAAGGCAICTCTCGITAIGCTITIGC 	1201 GAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAACCAAGTTATCAAAACAAGAGG 1260 1260 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAAAAGAGG 1319 1261 TGTTTCACACACTTTAAAAAAAAAAAAAAAAGAAATTGCTCCTCGTGACCAAGAATTTA 1320 1320 TGTTTCACACACTTTAACTGCTAAAAAAAAAAATGTTGCTCCTCGTGACCAAGAATTTA 1320	1321   TGATAAAGCATATAATGTGAAGGCTCATAAAGCCTTGTTGAAAATAAGGGTCG   1380	CAGAGCG	AGCTGATAAGTATCAACGTCAATGGTTACATTTTGATGAACAAGTGCGTATGCTTAATGAACAAGTGCTAATGCTTAATGAACAAGTGATAATCAATGGTTACATTTTTGATGAACATGGTTAATGATGAAAACATGGTTACATTTTTGATGAACATGGTATAATCAATGAAAAACATGGTTACATTTTTGATGAAACATGGAATTGGAAAAAAAGTTGGAATTGGAAAAAGCTTAATGGGCCATAGTCACTGGATTGGAAAAACCTCATATGGGCCATAGTCACTGGATTGGAAAAACCTCAATGGGCCATAGTCAGAAAAAAAA	1740 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1799

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GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John B.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus;
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-685
CURRENT APPLICATION NUMBER: US/10/412,862
CURRENT APPLICATION NUMBER: 09/468,656
PRIOR APPLICATION NUMBER: 09/468,656
PRIOR PLING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 9
LENGTH: 2451
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88 19 0.8 7493 15 US-10-187-319-5 GENERAL INFORMA 89 19 0.8 7493 15 US-10-131-510A-5 Sequence 5, Appli 90 19 0.8 91278 17 US-10-322-281-341 Sequence 341, App	RESULT 1 US-09-765-272-55 Sequence 55, Application US/09765272 Sequence 55, Application US/09765272 Patent No. US20020061545A1 GENERAL INFORMATION: TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key Mest Avenue CITY: Rockville	STATE: Maryland  COUNTRY: USA  ZIP: 20850  COMPUTER READABLE FORM:  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  COMPUTER: HP Vectra 486/33  OPERATING SYSTEM: MSDOS version 6.2  SOFTWARES ASCIT Text  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/09/765,272  FILING DATE: 2-Jan-2001  CLASSIFICATION: CURROWN:  PRIOR APPLICATION DATA:  APPLICATION DATA:  APPLICATION DATA:  APPLICATION OPTA:  APPLICATION DATA:  APPLICATION D	ATTORNEY/AGENT INFORMATION:  NAME: BROOKES, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8512 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 55: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: double STRANDEDNESS: double SEQUENCE DESCRIPTION: SEQ ID NO: 55: US-09-765-272-55	Query Match         100.0%; Score 2389; DB 9; Length 2389;           Best Local Similarity         100.0%; Pred. No. 0;           Matches 2389; Conservative         0; Mismatches         0; Indels         0; Gaps         0;           QY         1 TTCTTACGAGTTGGAACTGTATCAAGCTAAAGCAAATAATCGTGTTTCCTA         60           Db         1 TTCTTACGAGTTGGAACTGTATCAAGCTAAAGCGTAAGGAAATAATCGTGTTTCCTA         60           QY         61 TATAGATGGAAAAACAGCGAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA         120           QY         121 GCGTGAAAGAACAGCGAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA         120           QY         121 GCGTGAAAGAGCGAAACCTATCATTATACAATCGTCATCAAGACTATCATCACCAAGGCTATCTCC         180           QY         181 TTCACATGGCGACCATATCATTATTACAATGGTAAGGTTCCTTATGACGTTATCATCACC         180           QY         181 TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCACGG         240           QY         241 TGAAGAATTACTCATGATATACAATGGTAAGGTTCCTTATGACGCTATCATCACGG         240           QY         2241 TGAAGAATTACTCATGAAAAGTAAAGGTACCTTATGATCATCACGG         240           QY         2241 TGAAGAATTACTCATGAAAATAAAAGGTACCTTATGATCATCATGATGA         300

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(c) 1993 - 2004 Compugen Ltd
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Query Match

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Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 2347 AAAAGGAAGTAATCCTTCA 2365

Db 206 AAAAGGAAGTAATCCTTCA 224
Search completed: October 1, 2004, 03:35:56
Job time: 175 secs
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LOCATION: 408.7367
CTHER INFORMATION: /product= "Coagulation Factor VIII"
PUBLICATION INFORMATION:
                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SECTIVED STEER: BACCHILD Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/212,133A
FILING DATE: MATCH 11, 1994
CLEASSIFICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 7:
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CENTRALION FOR SEQ ID NO: 7:
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LOCATION: 7471...7476
OTHER INFORMATION: /function= "PolyA_signal"
FEATURE:
NAME/KEY: repeat_unit
LOCATION: 7368..7493
OTHER INFORMATION: /rpt_type= "terminal"
FEATURE:
FEATURE:
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RELEVANT RESIDUES IN SEQ ID NO:
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TYPE: nucleic acid
STRANDEDNESS: single
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ORIGINAL SOURCE:
ORGANISM: Mus musculus
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Matches 19; Conservative
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Gitschier,
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JOURNAL: Genomics
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                                                               APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Knechtle, Philipp
APPLICANT: Roeischung, Corinne
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, Corinne
APPLICANT: Rebischung, GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
APPLICANT: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 622
13;
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APPLICANT: Lollar, John S.
APPLICANT: Lollar, John S.
APPLICANT: RUNGE, Marschall S.
TILLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Kilpatrick & Cody
STREET: 100 Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFTCATION 7435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTONNEY/AGENT INFORMATION:
NAME: Wedisk, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.8%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 13; Matches 19; Conservative 0; Mismatches
Sequence 895, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08212133A
Patent No. 5663060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERINCE/DOCKET NUMBER:
REPERINCE/DOCKET NUMBER:
PF/S
TELECOMMUNICATION INFORMATION:
TELEPRONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 895:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          698 TCAAGAACAACTGGGTAC 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1559RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27709
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us-09-765-271-55.oli.rni

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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-961-527-192
                                                                                                                                Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic
STRANDEDNESS:
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                                                                                                                                                                                                      20850
                                                                                                                            STATE: Ma
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US-08-998-416-895
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Pakent No. 6420135
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | SEQUENCY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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100.0%; Pred. No. 0.037;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 24; DB 4; Length 134 Best Local Similarity 100.0%; Pred. No. 0.037; Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/961,083
FILING DATE: OCT-30-1997
ATTORNEY/ASTR INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 181:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 AIGCITAIACGTICCTCAIGGAG 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/09468656A; Patent No. 6582706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1342 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double
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Best Local Similarity 100.(
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-961-527-192/c
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US-09-468-656A-7
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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Score 24; DB 4; Best Local Similarity 100.0%; Pred. No. 0.039; Matches 24; Conservative 0; Mismatches 0
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0.8%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 4;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6492, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2368 TGTAAGTAAGGAAAAAATAA 2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6867 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14342
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STATE: Maryland

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Sequence 181, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
GENERAL TYPORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                               Sequence 181, Application US/08961083

Patent No. 6159469

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVATION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.0%; Score 24; DB 3; Length 1342; Best Local Similarity 100.0%; Pred. No. 0.037; Matches 24; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPRATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                               SEE: Human Genome Sciences, Inc.: 9410 Key West Avenue
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 ATGCTTATATCGTTCCTCATGGAG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1342 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                            STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-961-083-181
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RESULT 18
US-08-961-083-181
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                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
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Sequence 2, Application US/09468656A

Patent No. 6582706

GENERAL INFORMATION:

APPLICANT: Johnson, Leslie S.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

FILE REFERENCE: 468201-444

CURRENT APPLICATION NUMBER: 60/113,048

PRIOR APPLICATION NUMBER: 60/113,048

PRIOR PILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 14

SOSTWARRE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                       UPEKRALING SISIES.
SOFTWARE: ASCII TEXE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-0ct-1997
CLASSIFICATION NUMBER: US/09/536,784
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REPERENCE/DOCKET NUMBER: 99340P3
TELECOMMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 281:
SEQUENCE CHARACTERISTICS:
FUNCTH: 37 PASSE DAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Score 27; DB 100.0%; Pred. No. 0.(tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 281:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
       ZIP: 20850
COMPUTER READABLE FORM:
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Matches 27; Conservative
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US-09-468-656A-2
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LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Gaps

Page 10

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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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COMPUTER READABLE FORM:
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STRANDEDNESS: double
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US-08-961-083-281
                                                                                                                                                                                                                                                                             US-08-961-083-281
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Matches
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Sequence 3, Application US/09468656A

Sequence 3, Application US/09468656A

Sequence 3, Application US/09468656A

Sequence 3, Application US/09468656A

GENERAL INFORMATION:
APPLICANT: Adamou, John E.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: 1990-1-02

CURRENT APPLICATION NUMBER: US/09/468,656A

CURRENT APPLICATION NUMBER: 0/113,048

PRIOR APPLICATION NUMBER: 60/113,048

PRIOR FILING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 3: LENGTH: 40
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APPLICANT: Johnson, Jeslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-44
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR PLLING DATE: 1998-12-21
PRIOR PLLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 2.1
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CREANISM: Artificial Sequence
FEATURE:
CONGANISM: OTHER INFORMATION: Description of Artificial Sequence: Forward primer
CHER INFORMATION: used in amplification of the Sp36 gene sequence.
US-09-468-656A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Reverse primer OTHER INFORMATION: used in amplification of the Sp36 gene sequence.
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                                                                                                                                                 0; Indels
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                                                                                             Query Match
1.3%; Score 30; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 30; Conservative 0; Mismatches 0;
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1.3%; Score 30; LB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 30; Conservative 0; Mismatches
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; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 282: US-09-536-784-282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-468-656A-3
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                                                                                                                                                                                                                                                 APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
UNDMER OF SEQUENCE: 452
CORRESPONDENCE ADDRESS:
                                            0;
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         1.1%; Score 27; DB 4; Length 36; 00.0%; Pred. No. 0.00093;
                                          Indels
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100.0%; Pred. No. 0.00093;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                    STREET: 9410 Key West Avenue STATE: Maryland COUNTRY: US? 21P
Query Match
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 27; Conservative 0; Mismatches
                                                                                              10 TTCTTACGAGTTGGGACTGTATCAAGC 36
                                                                           1 TICTIACGAGIIGGGACIGIAICAAGC 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                             Sequence 281, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
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Sequence 282, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:

APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HV Vectra 486/33

OPENATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-Oct-1997

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
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1.3%; Score 30; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSER: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2360 CCTTCATCTGTAAGTAAGGAAAAATAAAC 2389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-10-197
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELLE S. MARKS
REGISTRATION NUMBER: PB340P3
TELECHONE: (301) 309-8504
TELEPAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                APPLICALLY
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE, DOCKET NUMBER: PB34:
TELECHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 282:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 40 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-961-083-282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-09-536-784-282/c
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                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCE: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
CONNIRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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| Sequence 282, Application US/08961083
| Patent No. 6159469
| GENERAL INFORMATION:
| TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
| CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
| CITY: Rockville | STATE: Maryland | STA
                                                                        1000 GCTCGTATTATTCCCCTTCGTTATCGTTCAACCATTGGGTACCAGATTCAAG 1052
                     983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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1.8%; Score 44; DB 4; Length 973;
Best Local Similarity 100.0%; Pred. No. 2.1e-12;
Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 CATTACCATTACÁTTCCTAAGAATGAGTTATCAGCTAGCGAGTT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 CATTACCATTACATTCCTAAGAATGAGTTATCAGCTAGCGAGTT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,527 FILING DATE: CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PELLORATION

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REPERSNEY/BOCKET NUMBER: PB340P1
TELEPHONE: (301) 309-8512
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
                                                                                                                                                                                                      RESULT 10
US-08-961-527-355
'Sequence 355, Application US/08961527
'Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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RESULT 8
US-09-468-656A-5
; Sequence 5, Application US/09468656A
; Patent No. 6582706
; GENERAL INFORMATION:
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US-09-468-656A-11
Sequence 11, Application US/09468656A
; Patent No. 6582706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                 983 GCTCGTATTATTCCCCT
                                                                                                             Query Match
Best Local Similarity 100.0
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 53; Conservative
                  TYPE: nucleic acid
STRANDEDNESS: double
                                                        TOPOLOGY: linear
                                                                           US-08-961-527-243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5
LENGTH: 2531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-468-656A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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100.0%; Pred. No. 5.4e-17;
tive 0; Mismatches 0; Indels
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
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COMPUTER READABLE FORM:
MEDIUM TYPE Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
                                                                       CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION OF A.
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 65:
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                                                                                                                                                                                                                                                                                                                                               309-8512
                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2290 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100./
Matches 53, Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
TITLE OF INVENTION: Motifs
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT APPLICATION NUMBER: 60/113,048
PRIOR PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1998-12-1
NUMBER OF SEQ ID NOS: 14
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APPLICANT: Johnson, Leslie S.

APPLICANT: Johnson, Leslie S.

APPLICANT: Adamou, John E.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

FILE REFERENCE: 469201-444

CURRENT APPLICATION NUMBER: US/09/468,656A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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2.2%; Score 53; DB 4; Length 2359;
100.0%; Pred. No. 5.4e-17;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.4e-17;
ive 0; Mismatches 0; Indels
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Sequence 65, Application US/09536784
Sequence 65, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TATLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                    Sequence 65, Application US/08961083
Sequence 65, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966
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                                2.2%; Score 53; DB 3; Length 2290;
100.0%; Pred. No. 5.4e-17;
iive 0; Mismatches 0; Indels
       2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAAATAAAC
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                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb is COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                       Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                               STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                  20850
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US-09-536-784-65
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                                                                                                      RESULT 5
US-08-961-083-65
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                                                                                                                                                                                                                         4492
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                                                                         4372
GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG 4312
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                                    TGTTTCACACACTTTAACTGCTAAAAAAAAAATGTTGCTCCTCGTGACCAAGAATTTTA
                                                                       1313 IGTÍTCACACACTITAACTGCTAAAAAGAAATGTTGCTCCTCGTGACCAAGAATTTTA
                                                                                                             TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG
                                                                                                                                              4373 IGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAAGCCTTGTTTGAAATAAGGGTCG
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Oy 2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGCTTGC	RESULT 4  US-08-961-527-94  i Sequence 94, Application US/08961527  i Patent No. 6420135  i GENERAL INFORMATION:  APPLICANT: Charles Kunsch  ITILE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  CORRESPONDENCE ADDRESS:  ADDRESSEE: Human Genome Sciences, Inc.  STREET: 9410 Key West Avenue  STREET: MANY and  STREET: MANY and	COUNTEY: USA  ZIP: 20850  COMPUTER READABLE PORM:  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  COMPUTER: HP Vectra 486/33  OPERATING SYSTEM: MSDOS version 6.2  SOFTWARE: ASCII Text  APPLICATION NUMBER: US/08/961,527  FILING DATE:  CLASSIFICATION: 424  PRIOR APPLICATION DATA:	APPLICATION NUMBER: FILING DATE: ATTORNEY AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REPERENCE/DOCKET NUMBER: PB340P1 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO. 94: SEQUENCE GHARACTERISTICS: LENGTH: 8195 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: double	mil CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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Set Local Similarity 100.00; Pred. No. 0; o, indels 0; deps 0; acches 2389; Conservative 0; Mismatches 0; indels 0; deps 0; conservative 0; Mismatches 0; indels 0; deps 0; conservative 0; mismatches 0; deps 0; conservative 0; deps	qa 2	qa .	රු පු	δ	a &	୍ ପୁ	7 A 6	à d	8 B 8	3 8 8	3 A 8	QD QD	à 8 á	o da	A 8 6		Qy qn	\dagger \dagge	8	8 8	qa
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GCCAGTGAGCATGTGTTAGGCAAGAAGACCACAGTGAAGATCCAAAA CAACGTCAGATGCTTACATTTTTGATGAACATGATATAATCAGTGA ATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 3GGGAAAAAGGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA AAAAACGGTAATTTGATTACTTCCTCATAAGGATCATTACCATAATAT AADAACGGTAATTTGATTATTCCTCATAAGGATCATTACCATAATAT TTGATGATCACATACAAAGCTCCAAATGGCTATACCTTGGAAGA ATTANGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA SCCAGTGAGCATGTGTTAGGCAAGAAGACCACACAGTGAAGATCCAAA TAGATGATTTATTGGGATTCCTAGGACCAATTACCCATCCAGAGGG BAAAAAGTTGCAGCTCTATACTAAAGAAAAGGTATCCTACC AAGCCTTAGACAATTATTAGAACGCTTGAATGATGAATCGACTAA ATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT GCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG TAACTGCTAAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA

FEATURE:   FEATURE:     FEATURE:     NAME/EXT:     MANE/EXT:     1.2451.	1621 TGAAGGAGATGCATATGTAACGCCTCATATGGCCATAGTCACTGGATTGGAAAGGTAG 1680 1681 CCTTTCTGATAAGGAAAAAGCTTGCAGCTCAAGCTATCTAAAGAAAAGGTACC 1740 1681 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCTATACTAAAGAAAAGGTATCCTACC 1740 1681 CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740
; NUMBER OF SEQ ID NOS: 14 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 9 IENTH: 2451	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAAGTGA 1620 
	1501 ACTIGGCRAACCAAAITCTCAAAITGAGIAIACIGAAGACGAAGITCGIAITGCTCAAIT 1560 
TITLE OF INVENTION: VACCIDE COMPOSITIONS COMP ; TITLE OF INVENTION: Motifs ; TITLE OF INVENTION: Motifs ; FILE REFERENCE: 469201-444	1441 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCCAGCG 1500 
; GENERAL INCORMATION: ; APPLICANT: Johnson, Leslie S. APPLICANT: Johnson, Leslie S. APPLICANT: Adamou, John B.	1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATGA
RESULT 3 US-09-468-656A-9 ; Sequence 9, Application US/09468656A	1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAATAAGGGTCG 1380 
OY 2341 GITGITAAAGGAAGTAATCCTTCATCTGTAAGTA DD 2341 GITGITAAAAGGAAGTAATCCTTCATCTGTAAGTA	1261 TGTTTCACACACTTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 
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2221	1141 ACGAAAAGTTGGGGAAGATATGTATTCGAAGAAAAGGGCATCTCTGTTATGTCTTTGC 1200 
2161	1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140 
2101	1021 GGTACCAGATTCAAGGCCAGAACAAGTCCACAACGGACTCCGGAACCTAGTCCAGG 1080 
Qy 2041 TGGATGGGGCAATGCCAGTGAGCATGTTAGGC	961 GTCTGAATTGGAAGAACGAATGGCTCGTATTATTCCCCTTCGTTATGGTTCAAACCATTG 1020 
Qy 1981 TITGTTGCGACGATTAAGTACTACGAACACC  [	901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 
1921	841 TCAACGACAIGTAGAATCTGATGGCCTTGTCTTTGATCCAGGACAATCACAAGTCGAAC 900 
Qy 1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATT  Db 1861 TACAGTTGAGGTTAAAAACGGTAATTTGATTATT	781 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG 840 
Qy 1801 CAATCGTGAAAGGGGAAAAACGAATTCCACTCC Db 1801 CAATCGTGAAAGGGGAAAAACGAATTCCACTC	721 TGTAAGCAATCCAGGAACTACAAATACTAACAAGGCAACAACAGCAACAGCAACAGTCA 780 
Qy 1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCA Db 1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCA	661 TTCAAGAACCTATGGCGACAAAATAGGGATAACACTTCAAGAACAAACTGGGTACCTTC 720 

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                 OPERATING SYSTEM: MSDOS version 6.2
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Pred. No. 0;
); Mismatches
                                                                APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                              APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
 COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                     TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                         LENGTH: 2389 base pairs
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                               SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 2389; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland
COUNTRY: USA
ZIP: 2086
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 55, Application US/09536784 Patent No. 6573082 GENERAL INFORMATION:
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US-09-536-784-55
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                        pneumoniae Antigens and
                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
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.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                       E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 96,373
REFERENCE/DOCKET NUMBER: 98140P2
TELECOMMUNICATION INPORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INPORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDOS version 6
SUFTWARE: ASCIT TEXE
SUFTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                             ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                        STREET: 9410 Key CITY: Rockville STATE: Maryland COUNTRY: USA
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Best Local Similarity
Matches 2389; Conserv
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US-08-961-083-55
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.. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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.. /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
.. /cgn2_6/ptodata/2/ina/B_COMB.seq:*
.. /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
.. /cgn2_6/ptodata/2/ina/PacTuS_COMB.seq:*
                            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-961-57-243

US-09-468-656A-5

US-09-468-656A-1

US-09-468-656A-1

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/lab host="E" coli strain XL10-Gold, T1-resistant, F-"
/lab host="E" coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: FWD42nv; Purified genomic DNA from
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
/http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated by seared
ligated to definase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AR129022.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XI10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Pax: 81-45-503-9216
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0; Indels
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URL:http://genome.gsc.riken.go.jp/
organism="Mus musculus"
                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0203J06"
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Ltoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

Wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, M., Tanaka, T., Matsunia, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for emonine Picario.
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/clone_lib="RIKEN full-length enriched, 16 days neonate
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ve 0; Mismatches 0; Indels
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Job time : 6095 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="G630051N24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e mouse tissues.
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Matches 20; Conservat
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAP2 (gel 4732114|gbl_AP12977.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLU-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
84112, USA
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

1 (bases 1 to 267)
1 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Miderhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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2M0203J06R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
                                                                                                                                                                                          /lab host="E. Coli strain XLI0-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Pred. No. 2e+02;
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Fax: 801 585 7177
Email: ddunngenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: J column: 06
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                        organism="Mus musculus"
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Location/Qualifiers
                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                             'db xref="taxon:10090"
                                                                                                                                      clone="UUGC1M0571J01"
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Best Local Similarity 100.0%; P:
Matches 20; Conservative 0;
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                                                                                                                                                                       sex="Male
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source
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                                                                                                                                                                                          /lab hose="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Weator: PWD42nv; Purified genomic DNA from M.
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources (Jacuments/duares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifica at constant velocity. The sheared DNA
was blunt ende repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ende in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adapprored vector DNA, and transformed into
chemically-competent E. coli Xili0-Gold (Stratagene) cells
and selected for ampicillin resistance."
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S Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Mennen, E., Pedersen, T., Noes, M., Rose, M., Rose, R., Tingey, A.; von Niederhausern, A. and Wright, D., Waiss, R. Tingey, A.; von Niederhausern, A. and Wright, D., Waiss, R. Unpublished (2000)

L Unpublished (2000)

Contact: Robert B. Waiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Rose, M. Research Bldg., 20 S. 2030 E., SLC, UT
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1M0571J01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0571J01 F, genomic survey sequence.
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Insert Length: 10000 Std Error: 0.00
Plate: 0571 zow: J column: 01
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
                           organism="Mus musculus"
                                                         "mol type="genomic DNA"
'strain="C57BL/6J"
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Location/Qualifiers
                                                                                                                'db_xref="taxon:10090"
clone="UUGC1M0341023"
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Mus musculus
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Matches 20; Conservative
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Fax: 801 585 7177
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84112, USA
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AZ502341/c
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URL:http://genome.ges.riken.go.jp,
URL:http://genome.ges.riken.go.jp,
Carning.p., Nashiyama.y., westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,X., Okawa,W., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to Notl adapters, digested with ECORI, size-selected, and cloned into the Notl and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawaryous, mecasos, contracts; Crantats; Vertebrats; Euteleostom; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 175)

I (bases 1 to 175)

S (Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Itoh, M., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Kadowa, H., Kadowa, H., Kadowa, T., Ishii, Y., Ishikawa, T., Itoh, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Mixi, R., Mizuno, Y., Nakamura, M., Oda, H., Shibata, Y., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Shiraki, T., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB538572 RIKEN full-length enriched, 0 day neonate eyeball Mus musculus cDNA clone E130012112 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXECUTION OF STATE (Konno, H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 21; DB 13; Length 935;
100.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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JOURNAL
COMMENT
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BB538572
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SOURCE
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/note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGGGGGGGGAACTGGAGTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS 05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (228)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R., Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1M0341023F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0341023 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                             /clone lib="RIKEN full-length enriched, 0 day neonate eyeball" ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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100.0%; Pred. No. 2e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                 /tissue_type="eyeball"
/dev_stage="0 day_neonate"
/lab_host="DH10B"
                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 0341 row: O column: 23
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 bp
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Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                   Location/Qualifiers
1. .175
                                                                                                                                                                                                      /clone="E130012112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 TTTCCTATATAGATGGAAAA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 TTTCCTATATAGATGGAAAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ502341
AZ502341.1 GI:10683573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="bH108"
/clone_lib="CSRQCHNS3"
/note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
BCORI; Site_2: Not1; This normalized library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU273390 935 bp mRNA linear EST 26-NOV-2002 603531527F1 CSEQCHN53 Gallus gallus cDNA clone ChEST486f8 5', mRNA
                                                          9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

1 (bases 1 to 935)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
                                                                                                                                                                                                                                                                              28; Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO Box 88, Manchester, M60 10D, UT Tel: 01612/008930 Fax: 01612/360409 Email: Simon.Hubbard@umist.ac.uk. Location/Qualifiers
Contact: Brendan Loftus
Department of Bukaryotic Genomics
TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9031"
/clone="ChEST486f8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1242
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 TGTTAAAATCTTGAAAGCAA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Scc
ilarity 100.0%; Pr
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1222 TGTTAAAATCTTGAAAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .935
                                                                                                                                                                                                                                                                   . .870
                                                                                                                                                                                                    Seq primer: SP6
Class: BAC ends.
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ORGANISM
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LOCUS
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JOURNAL
MEDLINE
PUBMED
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="adult"
//dev stage="adult"
//deb_host="nbH10B"
//clone_lib="cospCcHK0"
//clone_lib="cospCcHK0"
//note="Organ: hearty Vector: pBluescript II KS(+); Site_1:
//note="organ: hearty Vector: pBluescript II KS(+); Site_1:
//note="organ: hearty Vector: pBluescript II KS(+); Site_1:
//note="organ: hearty Vector: pBluescript closes: cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
// Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
CCOMPAIDLE STREAM CONTONE ADDITIONAL OF THE PRIMERS OF THE
pBluescript (KS+) vector: The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9323 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
                                                                        1 (bases 1, to 799).

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W. T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 16-APR-2003
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotā; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D. End sequencing of Aedes aegypti BACs Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

0.9%; Score 21; DB 13; Length 799;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CSU-K33r.8E23, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aedes aegypti (yellow fever mosquito)
Aedes aegypti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'mol_type="mRNA"
'strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                    PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                               Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        870 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:9031"
'clone="ChEST504c11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2190 AACTCAAAGAAGCAGAAGTTT 2210
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CC088871.1 GI:29944500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Female"
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1 (bases 1 to 870)
             Gallus gallus
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DEFINITION
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AUTHORS
TITLE
JOURNAL
             ORGANISM
                                                                                                                                                                                    JOURNAL
MEDLINE
PUBMED
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KEYWORDS
                                                                                                                       AUTHORS
                                                                                                   REFERENCE
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Bosch, E.,

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Gaps

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RIGIN

RESULT 16 BU115421/c DEFINITION

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ORGANISM

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS

JOURNAL MEDLINE

TITLE

PUBMED

FEATURES

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/ Lissue type="whole embryo"

/ dev stage="20-21"

/ dev stage="20-21"

/ dev stage="20-21"

/ done_lib="CSEQCHNO3"

/ clone_lib="CSEQCHNO3"

/ clone_lib="CSEQCHNO3"

/ clone="Organ: whole embryo; Vector: pBluescript II KS(+);

Site_l: EcoRi; Site_2: Noti; This normalized library was

constructed from imilion independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blutted, ligated to NotI adapters, digested with

ECORI, size-selected, and cloned into the NotI and ECORI

compatible sites of a custom modified MCS of the

pBluescript (KSt) vector: The library was normalized in 2

rounder in a compatible contains the contained contained
                                                                                  BU211482 769 bp mRNA linear EST 25-NOV-2002 604159635F1 CSEQCHN03 Gallus gallus cDNA clone ChEST1013e10 5',
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Passianinae; Gallus.

I (bases 1 to 769)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rounds using conditions adapted from Soares tal., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 13; Length 769;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="white Leghorn, Hisex"
/db_xref="taxon:931"
/clone="ChEST1013e10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 70;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PO Box 88, Manchester, M60 1QD, UK
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/organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Gallus gallus
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Gallus gallus (chicken)
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Best Local Similarity 100.0
Matches 21; Conservative
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Fax: 01612360409
                                                                                                                                                            mRNA sequence.
BU211482
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       RESULT 17
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/dev_stage="adult"
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/clone_lib="CSEQCHL15"
/clone_stage="order"
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/clone_stage="order"
/clone_stage="order"
/cloned protocol (Construction of pBluescript II KS(+); Site 1:
/crimmed protocol (Construction of uni-directionally
/cloned cDNA libraries from messenger RNA for improved
/cloned cDNA libraries from descript II KS(+) with NotI and EcoRI.
/close in double stranded adaptor containing Bsgl and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU115421 754 bp mRNA linear EST 25-NOV-2002 603140883F1 CSEQCHL15 Gallus gallus cDNA clone ChEST132e22 5', mRNA
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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University of Manchester Institute of Science and Technology
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                                                                                                                 13; Length 742;
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100.0%; Pred. No. 70;
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reannealing hybridization was used."
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                                                                                                 0.9%; Score 21; DB
ilarity 100.0%; Pred. No. 70;
Conservative 0; Mismatches
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Conservative 0; Mismatches
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/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST132e22"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                              2190 AACTCAAAGAAGCAGAAGTTT 2210
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Gallus gallus
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                                                                  Query Match
Best Local Similarity
Local 21; Conserva
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Best Local Similarity
Matches 21; Conserv
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Gaps

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Best Loca Matches

DRIGIN

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/dev stage="dath:"
//dev stage="dath:"
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/clobe_lib="CSEQCHN54"
/clobe_lib="CSEQCHN54"
/mote="Organ: brain; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded CDNA
was blunted, ligated to NotI adopters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KRs+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
Following this first strand reaction, double-stranded CDNA was blunted, ligated to NotI adapters, digested with ECORI, size-selected, and cloned into the NotI and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996). 791, except that a significantly longer reannealing hybridization was used."
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J..
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                 Gaps
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST875k20"
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Fax: 01612360409
Email: Simon-Hubbard@umist.ac.uk.
Location/Qualifiers
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Gallus gallus
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/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

(bases 1 to 731)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Butt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU403931 731 bp mRNA linear EST 27-NOV-2002 604141302F1 CSEQCHN59 Gallus gallus cDNA clone ChEST974d2 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                            /clone="bages35c04"
/tissue_type="shoots"
/dev_stage="germination"
/clone_lib="K, Sato unpublished cDNA library, cv. Haruna
Nijo germination shoots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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University of Manchester Institute of Science and Technology
(UMIST)
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                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1118 11-559-81-6856
Fax: 81-559-81-6855
Email: tshiniogenes.nig.ac.jp.
10-cation/Qualifiers
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/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 70; Matches 21; Conservative 0; Mismatches
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Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                           sub_species="vulgare"
db_xref="taxon:112509"
                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/cultivar="Haruna Nijo"
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/clone="ChEST974d2"
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/lab_host="DH10B"
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             Tadasu Shin-i
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                   Contact:
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Pan troglodytes
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BJ549886
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R.Site 1 : SacI
R.Site 2 : SacI.
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Matches 21; Conserv
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/dev stage="derebellum"
/dev stage="dult"
/lab_host="Nath10"
/clone lib="CSEQCHN68"
/clone lib="defend libit lib lib="defend lib-"defend lib-"defend lib-"defend lib-"defend lib-"defend lip-"defend libit libit lib-"defend libit libit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU345704 664 bp mRNA linear EST 28-NOV-2002 604170839F1 CSEQCHN68 Gallus gallus cDNA clone ChEST1033ml0 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1. (Dases 1 to 664)

Boardman, P. E., Sanz-Ezquerro, J., Cverton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology
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100.0%; Pred. No. 69;
                 0.9%; Score 21; DB 28; Length 640;
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/mol type="mRNA"
/strain="Compton Line 151"
/db xref="taxon:9031"
/clone="ChEST1033m10"
Query Match

Outlier (1) Outlier (2) Outlier (2) Outlier (2) Outlier (3) Outlier (3) Outlier (4) Outlier (4) Outlier (5) Outli
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Conservative 0; Mismatches
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Tel: 0.015.12008930
Fax: 0.1612360409
Email: Simon.Hubbard@umist.ac.uk.
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1. .664
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source

FEATURES

MEDLINE PUBMED

COMMENT

JOURNAL

TITLE

AUTHORS

REFERENCE

VERSION KEYWORDS SOURCE ORGANISM

LOCUS DEFINITION BU345704/c

RESULT 11

ACCESSION

Query Match

ORIGIN

Best Loca Matches

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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokchama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, WEL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9111, Fax:81-45-503-9111, Fax:BL-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
GSS 03-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 14-NOV-2002
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases I to 690)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
AGO84591 681 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-082G04.F, genomic survey sequence.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Logilyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                       Fujjyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Query Match
Best Local Similarity 100...
Loca 21; Conservative
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Fax: 801 585 7177
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ORGANISM
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                                                                                                                                                                                                                                          RESULT 10
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//dev stage=radult"
/lab host="DH10B"
/loce=11b=CSEQCHNS9"
/note=="Organ: small intestine; Vector: pBluescript II
/note="Organ: small intestine independent clones.

CDMA synthesis was initiated using an oligo(dT) primer,

Using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Notl adapters, digested with
ECORI, size-selected, and cloned into the Notl and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., DNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 581)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                          /clone_lib="NotreDame Liverpool-9714"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
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                                                                                                                                                                                                                                                                                         Gaps
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University of Manchester Institute of Science and Technology
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                                                                                          0.9%; Score 21; DB 29; Length 551; .00.0%; Pred. No. 68;
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/mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db xref="taxon:9031"
                           xref="taxon:7159"
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                                                                                                                                                                                                                                                                                                                                                                        27 IGITAAAAICTIGAAAGCAA 7
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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manche
Tel: 01612008930
Fax: 01612360409
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                                                                                                                                                                                                                                                         Best Local Similarity Matches 21; Conserv
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BU397983.1
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KEYWORDS
SOURCE
ORGANISM
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TITLE JOURNAL MEDLINE PUBMED

COMMENT

FEATURES

ORIGIN

REFERENCE

BU397983/c

RESULT 9

ACCESSION

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (gil#132114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coll X110-Gold (stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                             A640 bp DNA linear GSS 03-OCT-2000 1M0153A03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGCIM0153A03 R, genomic survey sequence.
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XLJO-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UJGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                    Gaps
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Score 21; DB 13; Length 581;
                                                                    0; Indels
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                             100.0%; Pred. No. 68; ive 0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone="UUGC1M0153A03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 6
Location/Qualifiers
                                                                                                                                         2190 AACTCAAAGAAGCAGAAGTTT 2210
                                                                                                                                                                                 368 AACTCAAAGAAGCAGAAGTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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Unpublished (2000)
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Email: entagrigr.org
Library was provided by David Severson
Seq primer: SP6
Class: BAC ends.
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/strain="liverpool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4081"
/clone="clEF47b13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="TA496"
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                                                                                                                                                 Unpublished (1999)
Contact: CUGI
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/Lisaue type="hippocampus"
/Lisaue type="hippocampus"
/Lisaue type="hippocampus"
/Lisaue type="hippocampus"
/Lisaue type="hippocampus"
/Lione lib="NHH MGC 95"
/Lione lib="NHH M
                                                                                       EST 05-SEP-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 549)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Prarayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Inforte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1720 row: f column: 06
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 499) MNH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                             603242619F1 NIH_MGC_95 Homo sapiens CDNA clone IMAGE:5284997 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.
Matches 21, Conservative
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CC847187

NDL.9714.SP6 Notre Dame Liverpool Aedes aegypti genomic clone NotreDame Liverpool-9714, genomic survey sequence.
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="fruit pericarp"

dev stage="mature green (3-5 days pre-ripening)"

/lab_host="SOLR"

/clone_lib="tomato fruit mature green, TAMU"

/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:

Xhol; cLEF - Fruit were tagged at the lcm stage and

harvested 3-5 days prior to ripening. Fruit were cut in

half to verify the seeds were indeed 'immature' and the

seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aedes aegypti
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                           Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: https://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.9%; Score 21; DB 10; Length 549;
100.0%; Pred. No. 68;
iive 0; Mismatches 0; Indels
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Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC and sequencing of Aedes aegypti
Unpublished (2003)
Other GSSs: NDL.9714.T7
Contact: Brendan Loftus
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 549
/organism="Lycopersicon esculentum"
                                                                                             Giovannoni, J. Generation of ESTs from tomato fruit tissue
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Best Local Similarity 100.0
Matches 22; Conservative
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                                                                   Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA dleaved with BamHI
and KhoI was ligated to modified Lambda FLC-I vector (Carninci et
al., submitted for publication) digested with BamHI and Sall.
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH970231 682 bp DNA linear GSS 02-OCT-2002 odf81d11.bl B.oleracea002 Brassica oleracea genomic, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 682)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Mush,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpubblished (2002)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="B.oleracea002"
/lote="Vector: pGYWa13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mixture of silique and flower"
/lab host="DH10B"
/clone lib="RAPL15"
/note="Site_1: BamH1; Site_2: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 618;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
Mashington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: odf81 row: d column: 11
Seq primer: -21UPpOT forward
Class: shocgun
High quality sequence start: 14
High quality sequence stop: 519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                           /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Brassica oleracea"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 22; DB
llarity 100.0%; Pred. No. 21;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   clone="RAFL15-41-A11"
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ВН970231.1 GI:23453048
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nes 22; Conserv
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Matches
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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a

ORIGIN

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/dev stage="adult"
//dev stage="adult"
/lab host="DH10B"
/clon=11b="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded CDNA
was blunted, ligated to Not1 adapters, digested with
ECORI; size-selected, and cloned into the Not1 and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 92289932 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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0
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Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W. T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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100.0%; Pred. No. 66;
Lve 0; Mismatches 0; Indels
            DB 28; Length 682;
21;
                                                                      0; Indels
0.9%; bcc.
100.0%; Pred. No. c...
... 0; Mismatches
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/mol_type="mRNA"
/strain="Layer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="taxon:9031"
/clone="ChEST262f5"
                                                                                                                                    1811 AAAGGGAAAAACGAATTCCAC 1832
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                                                                                                                                                                                            44 AAAGGGAAAAACGAATTCCAC 23
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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CE751062/c LOCUS DEFINITION

RESULT 1

778 779 880 887 888 888 889

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

MEDLINE PUBMED COMMENT TITLE JOURNAL

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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Speamatophyta; Varidiplantae: Streptophyta; Embryophyta; Tracheophyta; Speamatophyta; Magnoliophyta; eudicotsleotyledons; core eudicots; 10soids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Hlarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil 20567808

Illispre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU236995 AFELIS Arabidopsis thaliana cDNA clone RAFLIS-41-A11 5',
                                                                                                                                                                                                                                                                                                                                                                                                   Email: bening@msu.edu
Clones were originally prepared at Michigan State University.
Arabidopsis Biological Resource Center, The Ohio State University,
309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210
USA, FAX: 6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
                                                                                                                                                                                                                                                                     Contact: Benning, C
Dept. of Blochemistry & Molecular Biology
Michigan State University
224 Blochemistry, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 22; DB 10; Length 261;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="seed"
/dev_stage="5-13 days after flowering"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 19;
Matches 22; Conservative 0; Mismatches
                       Arabidopsis thaliana (thale cress)
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/clone="600037123R1"
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Fax: 517 353 9334
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AUTHORS
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JOURNAL
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                                                                                                                 REFERENCE
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               CG862220 ZMMBBC027
BQ712408 AGENCOURT
CG858044 ZMBBC026
AK037912 Mus muscu
BH907885 SALK 0446
CC021347 3591 1 24
H74951 359 Random-
CE57072 tigr-gss-
BE505229 dc19909.x
BH867080 hg93b06.y
AV236691 AV236691
CF765303 CES002228
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BE528097
BE528097.1 GI:9786075
                                                                                                                                                                                                                                                                                                                                                                 tigr-gss-dog-17000369611786 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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   602301896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canis familiaris (dog)
Canis familiaris
Canis familiaris
Eukaryotz, Metzaog, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 469)
Kirkness, E. F., Bafna, V., Halpern, A. L., Levy, S., Remington, K., Rusch, D. B., Delcher, A. L., Pop, M., Wang, W., Fraser, C. M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
   BG033498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                   BE505229
BH867080
AV236691
                                                                       AK037932
BH907885
CC021347
H74951
CE567072
                                       BQ712408
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                                                         CG858044
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Matches 23; Conservative
 923
924
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BU473013 603365019 BI544663 603242619 AW932312 EGT358055 CC847187 NDL.9714.	BU397983 603534550 AZ391393 1M0153A03 BU345704 604170839	AG084591 Pan trogl BJ549886 BJ549886 BU403931 G04141302 HT033404 603869178	BU115421 603140883 BU211482 604159635 BU30827 603588542	CC008001 C301. BU273390 603531527 BB538572 BB538572 x750341 1M0341073	AZ302341 IM0341023 AZ769909 IM0571J01 AZ943045 ZM0203J06	BB803034 BB803034 CG109167 PUKDL80TB	AQ216823 HS 3253 B	BZ685217 PUBCP45TD AW239782 ptilc.pk0 CK229737 702668904	CF256901 pha004 c0 BH369198 AG-ND-139	CE778613 tigr-gss- BH766941 BMBAC345E	CK229735 702482441 CA370410 650577 NC BW303010 BW303010	BW282910 BW282910 CK229736 702568991 AZS24614 234PbD06	AQ412913 RPCI-11-1 BH765160 BMBAC354A	BW112810 BW112810 BW243771 BW243771	BG698682 602703065 BF296373 036PbB02	BH085526 RPCI-24-2 AZ373971 IM0126P17	BW261677 BW261677 BG911162 602806563	CE140831 tigr-gss- AJ453442 AJ453442	BW262397 BW262397 BF294340 004PbA08	BB527573 BW027074 BW027074	CK229738 702668904 AV862261 AV862261	CA763329 BR060002B CG851011 ZMMBBb033	AL141617 Anopheles CG098656 PUIME15TD	BW132597 BW132597 BZ995097 PUDFB72TD	BW131850 BW131850 AL150861 Anopheles	CBS98673 AGENCOURT BE130716 L48-922T3	BH374713 AG-ND-161 RJ566263 RJ566263	CC159651 ig03c07.g CC577803 CH240 456	BH045505 RPCI-24-3	AL440694 T3 end of CF255654 mdvn.130_e CG109169 PUKDL80TD	ıdvn.136
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	ic search, using sw model	September 30, 2004, 22:20:23; Search time 6083 Se (without alignments) 11727.889 Million cell	US-09-765-271-55 2389 1 TICTIRGGAGTIGGGACTGTTAAGTAAGGAAAAAAAAAA	OLIGO_NUC Gapop_60.0 , Gapext 60.0	27513289 segs, 14931090276 residues		hits satisfying chosen parameters: 55026578	length: 0 length: 200000000	: Listing first 90 summaries	EST:* : em estba:*		: em_estmu:* : em_estmov:*		: gb_est1:*	1: 95_htc:* 2: qb_est3:*		5: em_estfun:* 5: em_estom:*			1: em_gss_fun:* 2: em_gss_fun:* 2: em_gss_fun:*	em gas	em_gas	7. em gss kug: 7. em gss kug: 8. or gs 1.*	o: gb_gss1:*	results predicted by chance	greater than or equal to the score of the result being derived by analysis of the total score distribution.	SUMMARIES	<b>.</b>	Length DB ID	1.0 469 29 CB751062 CB751062 0.9 261 10 BB528097 BB528090	682 28 BH970231
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Brodeur B;

Martin D,

Charland N,

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New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1113 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1165
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                                                                                           19-JUN-2001; 2001WO-CA000908.
                                                                                                                               20-JUN-2000; 2000US-0212683P
                                                                                                                                                                     (SHIR-) SHIRE BIOCHEM INC
                                                                                                                                                                                                           Hamel J, Ouellet C,
                                                                                                                                                                                                                                               WPI; 2002-122272/16.
P-PSDB; AAU75934.
                 WO200198334-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-11-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product = "BVH-11-2"
/note = "The gene is flanked by sequences from the vector
SP64, no information on which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                     Streptococcus pneumoniae, BVH-3; BVH-11; BVH-28; antigen, vaccine, prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes nucleic acids (I) encoding protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcal antigens useful for vaccinating against e.g. otis media, bacteremia and/or pneumonia.
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                                                                                                                                                                                                                                                                                                                                                                                     Rioux C,
                                     Streptococcus pneumoniae BVH-11-2 gene SEQ ID NO:13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%; Score 53; DB 100.0%; Pred. No. 6.8
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                                                                                                                                                                                                                                                                                                                                                                                     Pineau I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK15104 standard; DNA; 2639 BP
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                                                                                                                                                                                                                                                                     99WO-CA001218
                                                                                                                                                                                                                                                                                                           98US-0113800P
                                                                                                                                                                                                                                                                                                                                               (BIOC-) BIOCHEM PHARMA INC.
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                                                                                                                                                       Streptococcus pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                     Brodeur BR,
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                         WO200039299-A2
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   21-NOV-2000
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The invention describes an isolated polypeptide (I) with 70-90% identity to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or burning to a sequences derived from them. A vaccine (II) comprising (I) is useful for therapeutic or prophylactic treatment of comprising (I) is useful for therapeutic or prophylactic treatment of midividual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A streptococcus such as Streptococcus properties, S. uberis, S. nocardia or Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nocardia or Staphylococcus aureus) in an individual susceptible to the infection. A copynuclectide (III) encoding (I) is useful in DNA immunisation test for S. pneumoniae infection. (III) is useful in DNA immunisation cortest for supermoniang the presence of Streptococcus in a biological sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonian uncleic acid in a sample for diagnosing streptococcal infections. This sequence encodes the antigenic streptococcus pneumoniae protein BVH-11-2, used to create the antigenic copynides described in the method of the invention
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100.0%; Pred. No. 6.8e-16;
iive 0; Mismatches 0; Indels
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Example 3; Fig 5; 113pp; English.
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BP.

AAA47602 standard; DNA; 2531

AAA47602

(first entry)

20-OCT-2000

AAA47602;

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Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody addincted against these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating bneumococcal infections which includes otitis media, nasopharyngeal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins.
1003 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1055
                                                                                                                                                                                                                                               Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2531 BP; 861 A; 508 C; 550 G; 609 T; 0 U; 3 Other;
                                                                                                                                                                                                               Recombinant variant of Sp36 gene (Sp36B) of S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                               'product= "Sp36B polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 69-70; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adamou JE;
                                                                                                           AAA47605 standard; DNA; 2531 BP
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                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIMMUNE INC
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P-PSDB; AAB01469.
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                                                                                                                                                                                20-OCT-2000
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                                                                                                                                             AAA47605;
                                                                        RESULT 22
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Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HxxHxH) or a coiled-coil region, or an antibody against these features. The vaccine is useful in protecting against these features are pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating pneumonoccal infections which includes otitis media, nasopharyngeal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins.
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                                                                                                                          Streptococcus pneumoniae; infection; vaccine; coiled coil region; histidine triad residue; Sp36; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis;
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100.0%; Pred. No. 6.8e-16;
                                                                                              Recombinant variant of Sp36 gene (Sp36D) of S. pneumoniae.
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                                                                                                                                                                              meningitis; lobar pneumonia; ds
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/*tag= a
                                                                                                                                                                                                               Streptococcus pneumoniae.
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P-PSDB; AAB01466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AAA65737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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X
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0

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0; Gaps

0; Indels

DB 3; Length 2531; 6.8e-16;

ch 2.2%; Score 53; DB 1.1 Similarity 100.0%; Pred. No. 6.8 53; Conservative 0; Mismatches

Local Similarity

Best Loca Matches

à d

Query Match

1000 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1052

23

RESULT

983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG

Gene, ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.

Streptococcus pneumoniae; type 4 strain.

WO200277021-A2.

03-OCT-2002

27-MAR-2002; 2002WO-IB002163. 27-MAR-2001; 2001GB-00007658

S. pneumoniae type 4 strain coding region #993

(first entry)

(revised)

27-OCT-2003 11-FEB-2003

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AAYB1501 to AAYB1679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotide sequences can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAA05591 to AAA05614 represent primers used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcal protein, useful as a vaccine, for diagnosis of mococcal diseases and for screening agents capable of antagonizing or biting expression of the protein.
983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                   1003 GCTCGTATTATTCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1055
                                                                                                                                                                                                                                                                              Streptococcus pneumoniae, vaccine, screening, protein antigen; antibacterial, antiinflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2481 BP; 839 A; 514 C; 538 G; 590 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         Streptococcus pneumoniae nucleotide sequence ID311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Le:
6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.2%; Score 53; DB 100.0%; Pred. No. 6.8 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 99; 108pp; English.
                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MICR-) MICROBIAL TECHNICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-00016337.
99US-0125164P.
                                                                                                                               AAA05417 standard; DNA; 2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-GB002451
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oneumococcal diseases and
inhibiting expression of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.2
Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                   pneumococcal disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gilbert CFG, Hansbro PM;
                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-195300/17.
P-PSDB; AAY81662.
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19-MAR-1999;
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                                                                                                                                                                    AAA05417;
                                                                                            RESULT 20
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                                                                                                                AAA0541'
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useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or proteins and nucleic acid molecules from Streptococcus pneumoniae,

Fraser C;

Tettelin H,

Masignani V,

WPI; 2003-040579/03.

P-PSDB; ABU01418

New

(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified bNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the composition, a kit comprising first and second primers, which are the first primer is substantially complementary to the target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence to and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having contacting a test compound with the substantial complementary to define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic contacting or preventing a disease or infection due to streptococcus contacting a rear infection. They are also useful as medicaments for treating or preventing a disease or infection due to streptococcus immunodominant proteins. The present sequence is one of the 2489 immunodominant proteins. The present sequence is one of the 2489 immunodominant proteins. The present sequence is one of the 2489 immunodominal electronic formet discently from WiPO at this patent did not form part of the printed on 27-0CT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2517 BP; 830 A; 509 C; 545 G; 633 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 1985; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standardise OS field)
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Gaps ; Length 2517; 0; Indels 2.2%; Score 53; DB 7; L. 100.0%; Pred. No. 6.8e-16; iive 0; Mismatches 0; 53; Conservative Query Match Best Local Similarity Matches

8

. 0

Gaps

.; 0

0; Indels

à g ABX06705 standard; DNA; 2517 BP

RESULT 21 ABX06705 ID ABX0 XX AC ABX0

ABX06705;

983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035

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New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 Gaps
                    983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                1879 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1931
                                                                                                                                                                               Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
  ..
 Indels
 .
0
                                                                                                                                                              S. pneumoniae type 4 strain coding region #1173.
 0; Mismatches
                                                                                                                                                                                                                           Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; SEQ ID NO 2345; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                           Masignani V, Tettelin H, Fraser C;
                                                                                          ABX06885 standard; DNA; 2457 BP
                                                                                                                                                                                                                                                                                    27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                                                                                                          27-MAR-2001; 2001GB-00007658
                                                                                                                                           (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-040579/03.
P-PSDB; ABU01597.
                                                                                                                                                                                                                                              WO200277021-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ear infection.
                                                                                                                                27-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                  03-OCT-2002.
 53;
                                                                                                             ABX06885;
 Matches
                                                                     RESULT 18
                                                                                ABX06885
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the SESS6454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target the first primer is substantially complementary to the target sequence and where the parts of the primers having the target sequence or substantially complementary to the carget sequence of the target sequence and where the parts of the primers having the target sequence to he amplementary to the target sequence of the target sequence the parts of the primers baying the parts of the primers baying the parts of the primers baying the parts of the target sequence to the amplementary to the carget sequence to the amplified and agent of the parts of the primers baying the parts of the primers baying the parts of the primers baying the parts of the primer baying the parts of the primers baying the parts of the primers baying the parts of the primers baying the parts of the primer baying the parts of the parts of the primers to the parts of the primers baying the parts of the p be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, oitis media or ear infection. They are also useful in developing vaccines diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2489 identified coding region from the genomic sequence. Note: The sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human C3-degrading protein (see AAY91939) of about 92 kDa. This sequence may encompass a smaller 20 kDa polypeptide coding sequence (AAA08556) also having human C3-degrading activity. The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal Antibodies against the proteins can be used to inhibit S. pneumoniae mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the nucleic acid sequences on the surface of an organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are
     but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or colonization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide is used to stimulate immune system and immunize or treat a mammalian subject against Streptococcus pneumoniae infection or colonization.
data for this patent did not form part of the printed specification, was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                             983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                                                                                                                                                                      1000 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                     S. pneumoniae 92 kDa human C3-degrading protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human C3-degrading protein; 92 kDa; immunostimulatory; vaccine; inhibitor; inflammation; organ rejection; xenotransplantation;
                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence, isolated from Streptococcus pneumoniae,
                                                                                                                                2.2%; Score 53; DB 7; Length 2457; 100.0%; Pred. No. 6.8e-16; Live 0; Mismatches 0; Indels
                                                                                             Sequence 2457 BP; 836 A; 497 C; 531 G; 593 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2478 BP; 837 A; 510 C; 535 G; 596 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.2%; Score 53; DB 3; Length 2478;
100.0%; Pred. No. 6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masi AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 55-57; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MINU ) UNIV MINNESOTA.
(AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00283094.
                                                                                                                                                                                                                                                                                                                                          AAA08557 standard; DNA; 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US022362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0101736P.
                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hostetter MK, Finkel DJ,
                                                                                                                                                      Best Local Similarity 100.
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-283594/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200017370-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                                               AAA08557;
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                      RESULT 19
                                                                                                                                                                                                                                                                                                                        AAA08557
     8×30000
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...... acids. ABQ84905 to ABQ85130 represent primers used in the cloning of S. pneumoniae ORFs (open reading frames) which are used in an example from the present invention
                                                                                                                                                                                                                                            encoding the S. pneumoniae antigens can be used to detect Streptococcus nucleic acids. AB094905 to AB085130 represent primers used in the clonin
                                                         The S.
ABO84792 to ABO84904 represents nucleic acids which encode the Streptococcus pneumoniae antigens given in ABD84557 to ABD84669. The Spneumoniae antigens have antibacterial activity and can be used in vaccines. The S. pneumoniae antigens can also be used to prevent or attenuate a Streptococcal infection in an animal. The polynucleotides
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Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 0 U; 5 Other;

Gaps 0 Length 2290; 0; Indels 6.8e-16; 9 2.2%; bccc. 100.0%; Pred. No. e... ... 0; Mismatches Query Match
Best Local Similarity 100.
Matches 53; Conservative ð

RESULT 16

ADC45146;

ADC45146 standard; DNA; 2290 BP

(first entry) 18-DEC-2003

S. pneumoniae DNA encoding antigen SP042.

Antigen; ds; bacterial infection; vaccine; pneumonia; antibacterial:

Streptococcus pneumoniae

US6573082-B1.

03-JUN-2003

28-MAR-2000; 2000US-00536784

96US-0029960P 97US-00961083 31-OCT-1996; 30-OCT-1997; SCI INC. (HUMA-) HUMAN GENOME

Fannon MR; m Dougherty Dillon PJ, Kunsch CA, Barash SC, Rosen CA; Choi GH,

WPI; 2003-764574/72. P-PSDB; ADC45147 Novel polynucleotide encoding Streptococcus pneumoniae polypeptides useful for producing vaccines for prevention or attenuation of infection by Streptococcus pneumoniae.

Example 1; SEQ ID NO 65; 58pp; English.

The invention relates to an isolated polynucleotide consisting of a Streptococcus pneumoniae nucleic acid (appearing as ADC45122 and encoding Streptococcus pneumoniae nucleic acids encoding 113 S. pneumoniae antigens. Also included are making a recombinant vector by inserting the nucleic acid into a vector, an isolated polynucleotide consisting of at least 50 or 100 contiguous nucleotides of the SPO28 nucleic acid, and a recombinant host cell comprising the SPO28 polynucleotide. The nucleic acids are useful as DNA vaccine against Streptococcus pneumoniae infection (e.g. pneumonia). Nucleic acids derived from the S. pneumoniae antigen nucleic acids are useful as probes for use in diagnostic methods for detecting S. pneumoniae agene expression. The present sequence encodes an S. pneumoniae antigenic protein. ADC45146

ADC45146

XX

ADC4

XX

ADC4

XX

ADC4

XX

ADC4

XX

ADC4

AD

Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 0 U; 5 Other;

.; 0 Gaps ; 983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 944 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG Length 2290; Indels 6.8e-16; nes 0; DB 9; 2.2%; scc. 100.0%; Pred. No. c. ... 0; Mismatches Conservative Query Match Best Local Similarity Matches 53; Conserv g ò

AAV52376 standard; DNA; 2359 BP.

AAV52376;

6

(first entry) 23-OCT-1998 Streptococcus pneumoniae genome fragment SEQ ID NO:243.

pneumoniae; S. pneumoniae; genome; diagnosis; assay; ble medium; vaccine; pharmaceutical composition; ds. Streptococcus pneumoniae; computer readable medium;

Streptococcus pneumoniae.

W09818931-A2

07-MAY-1998

97WO-US019588. 30-OCT-1997;

96US-0029960P. 31-OCT-1996;

(HUMA-) HUMAN GENOME SCI INC

Fannon M; Barash SC, Dillon PJ, Rosen CA, Choi GH, Dougherty BA; Kunsch CA, 

WPI; 1998-272225/24.

Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae.

Claim 1; Page 1265-1266; 1409pp; English

The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus communicae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S. pneumoniae comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that by bridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating meNNA, DNA or DNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplifying nucleic acid molecules whose nucleotide sequence is communiae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in the computer or an expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in the computer and assays, and pharmaceutical compositions and vaccines

Sequence 2359 BP; 786 A; 451 C; 511 G; 611 T; 0 U; 0 Other;

2.2%; Score 53; DB 2; Length 2359; 100.0%; Pred. No. 6.8e-16; Query Match Best Local Similarity

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Claim 1; Page 28-29; 70pp; English
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Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection
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(DOUG/)
(FANN/)
(ROSE/)
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(BARA/)
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ABQ84824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneudoniae serotype that is capable of degrading human complement protein C3 (HCPC3). It was identified in the S. pneumoniae serotype 4 genome by alignment to another novel open reading frame (see AAX25393) that codes for a 20 kDa HCPC3 protease (AAY65752) of S. pneumoniae serotype 3. This suggested the open reading frame. Haino cards 1-58 and 90-132 of the 20 kDa protein have substantial sequence acids 170-227 and 258-300 of the 79 kDa protein. Proteins and peptides or polypeptides concaining these regions, and DNA sequences encoding them (nucleotides 507-681 and 827-999 of the present sequence) are claimed. HCPC3 proteases and polypeptides can be used as immune system stimulating compositions (claimed). They can produce an immune response against 5 pneumoniae to immunize or treat a mammalian subject against infection or colonization (claimed). They can produce a call response a T cell response, a claimed). The expression of the proteins on endothelial cell response (claimed). The expression of the proteins on the surface of an organ of an animal used in xenotransplantation can be used to inhibit C3-mediated inflammation and rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       688 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae, antigen; vaccine, infection; diagnosis; detection; pneumonia; otitis media; meningitis; ss.
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/transl_except= (pos:1406. .1408,aa:Xaa)
/transl_except= (pos:1430. .1432,aa:Xaa)
/note= "no stop codon given; Xaa is unspecified"
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                                                                                      protein (see AAY05753) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2163 BP; 737 A; 450 C; 462 G; 514 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Le..,
5. 6.8e-16; Indels
7. 7.34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 53; DB 100.0%; Pred. No. 6.8 tive 0; Mismatches
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    Claim 54; Page 52-54; 66pp; English.
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                                                                                      sequence encodes a 79 kDa
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P-PSDB; AAW55095.
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les 53; Conserv
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                                                                                                                                                                                                              be useful in vaccines for inducing protective antibodies against be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunosasys, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein are used to immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                              The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fannon MR;
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    or their epitope-containing fragments, useful in protective or
therapeutic vaccines, and for diagnosis.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2290 BP; 766 A; 474 C; 498 G; 547 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2290;
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Pred. No. 6.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (especially 10-300) mu g/ml per dose
                                                                                                Claim 1; Page 61-62; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ84824 standard; DNA; 2290 BP
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Best Local Similarity 100.
Matches 53; Conservative
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KUNSCH C A.
BARASH S C.
DILLON P J.
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Masi AW;

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The present sequence, isolated from Streptococcus pneumoniae, encodes a human C3-degrading protein (see AAY91938) of about 20 kDa. This sequence may be part of a larger open reading frame (see AAA08557) which encodes an approximately 92 kDa protein also having human C3-degrading activity. The DNA sequences can be used for producing an immune response to Streptococcus pneumoniae in a mammal. Antibodies against the proteins can be used to inhibit S. pneumoniae-mediated C3 degradation. C3-mediated inflammation and rejection in xenotransplantation can be inhibited by expressing the mucleic acid sequences on the surface of an organ of an animal. In particular, the polypeptides are useful for stimulating the immune system and are effective to immunize or treat a mammalian subject against Streptococcus pneumoniae infection or colonization
                                                                                                                                                                                                                                       Isolated polypeptide is used to stimulate immune system and immunize or treat a mammalian subject against Streptococcus pneumoniae infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human complement C3-degrading protease, vaccine, infection, meningitis, pneumonia, xerotransplantation, transplant rejection, inflammation, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            983 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 GCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTGGGTACCAGATTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae complement C3-degrading protease DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 3; Length 5v...
Pred. No. 6.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 504 BP; 153 A; 125 C; 98 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human complement C3-degrading proteinase.
                                                                                                                  Green BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Green BA,
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                                                                                                                  Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 53; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX25394 standard; DNA; 2163 BP.
                                            (MINU ) UNIV MINNESOTA.
(AMCY ) AMERICAN CYANAMID CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US020186
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99US-00283094
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                                                                                                                     Finkel DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MINU ) UNIV MINNESOTA
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Best Local Similarity
                                                                                                                                                                                          P-PSDB; AAY91938
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                                                                                                                     Hostetter MK,
31-MAR-1999;
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Dp
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                                                                                                                                                                                                                                                                               to Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or Streptococcus pneumonia protein BVH-3, BVH-11, variants of BVH-3 or comprising (I) is useful for therapeutic or prophylactic treatment of meningitis, office media, bacteraemia or pneumonia infection in an individual susceptible to these disorders. (II) is also useful for therapeutic or prophylactic treatment of any streptococcal bacterial infection (e.g., caused by Streptococcus pneumoniae, group A Streptococcus such as Streptococcus system of Streptococcus auchorance of Straphylococcus auchorance of Straphylococcus auchorance of Straphylococcus auchorance of Straphylococcus auchorance individual susceptible to the infection. A polymucleotide (III) encoding (I) is useful in DNA immunisation test for S: pneumoniae infection. (III) is useful for designing DNA probes for use in detecting the presence of Streptococcus in a biological
                                                                                            New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing polypeptides, useful as vaccine components for treating or preventing streptococcal infections such as otitis media, meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sample suspected of containing the bacteria. The DNA probes may also be used for detecting circulating S. pneumonia nucleic acid in a sample for diagnosing streptococcal infections. This sequence encodes the
                                                                                                                                                                                                                                                                The invention describes an isolated polypeptide (I) with 70-90% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae protein BVH-11, used to create the antigenic peptides described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     699 CAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. pneumoniae 20 kDa human C3-degrading protein coding sequence.
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Pred. No. 4.9e-64
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100.0%; Pred. No. *...
7. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCTCTACAACTGCCTTTGAGTCAACG 949
                                                                                                                                                                                                                   Disclosure, Fig 4, 113pp, English.
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Best Local Similarity 100.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae.
                        WPI; 2002-122272/16.
P-PSDB; AAU75933.
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                                                                                                                                                                       bacteremia
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Length 504;

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Hamel J, Ouellet C, Charland N,
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                                                                                                                                                                                                                                                                 Matches 148; Conservative
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           Brodeur BR,
                                 WPI; 2000-452397/39
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Best Local Similarity
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           Hamel J,
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                                                                                                                                                                                                                antigens (II) from Streptococcus monera. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens, may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-11 protein
                                                                                                                                                    Streptococcal antigens useful for vaccinating against e.g. meningitis, otis media, bacteremia and/or pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                 759 ACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                           758 CAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACAAGCA
                                                                                                                                                                                                                                                                                                                                                                                       CAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCA
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae; BVH-3; BVH-11; BVH-28; antigen; vaccine; prophylaxis; therapy; infection; diagnosis; meningitis; bacteraemia; otitis media; pneumonia; immunisation; bactericidal; ds.
                                                                                                                                                                                                           The present invention describes nucleic acids (I) encoding protein
                                                                                                Charland N;
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0
                                                                                                                                                                                                                                                                                                                                            Length 2523;
                                                                                                                                                                                                                                                                                                                     Sequence 2523 BP; 879 A; 523 C; 526 G; 595 T; 0 U; 0 Other;
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                                                                                               Martin D, Rioux C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae BVH-11 gene SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                           Score 148; DB 3; I
Pred. No. 4.9e-64;
                                                                                                                                                                                                                                                                                                                                   6.2%; Scc...
100.0%; Pred. No.....
0; Mismatches
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                                                                                                                                                                                     Example 2; Fig 3; 106pp; English
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                                99WO-CA001218
                                                      98US-0113800P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae
                                                                           (BIOC-) BIOCHEM PHARMA
                                                                                               Brodeur BR,
                                                                                                                     WPI; 2000-452397/39
                                                                                                                              P-PSDB; AAB12716
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                               20-DEC-1999;
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                                                      23-DEC-1998;
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          06-JUL-2000
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                                                                                               Hamel J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BVH-3; BVH-11; vaccine, meningitis, otitis media, bacteraemia, pneumonia, streptococcal bacterial infection; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                            may be used for the recombinant production of the proteins they encode. The protein antigens may then be used as vaccines for the prevention and treatment of Streeptococcal infections in mammals (especially humans) which result in, e.g. meningitis, otitis media, bacteraemia and/or pneumonia. The present sequence encodes the S. pneumoniae BVH-11 protein
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                                                                                                                                                                                                                                                                                                               antigens (II) from Streptococcus pneumoniae. The protein antigens have bactericidal activity. The nucleic acids, encoding the protein antigens,
                                                                                                                            Streptococcal antigens useful for vaccinating against e.g. meningitis, otis media, bacteremia and/or pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        759 ACAACAGCAACACTAACAGTCAAGGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAACAGCAACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTTTGAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 CAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                           present invention describes nucleic acids (I) encoding protein
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Charland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2647 BP; 934 A; 538 C; 556 G; 619 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martin D, Brodeur B;
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Rioux
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.2%; Score 148; DB 3;
100.0%; Pred. No. 4.9e-64;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding Streptococcus pneumoniae BVH-11
Martin D,
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Pineau I,
                                                                                                                                                                                                                           Example 6; Fig 15; 106pp; English
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	RESULT 9 AAA65731 standard; DNA; 2523 BP.  XX AC AAA65731; XX
481 AGGAGCCHATACTACAGATGATGATATATCTTTAATCCTTCGATATACATAGAGATAC 540 6410 AGGAGCCTATACTACAGATGATGATATATCTTTAATCCTTCGATATACATAGAGATAC 6411 6411 TGGAGATCTTAATCCTTCACGAGATCATACATACATACAT	1321 TGATAAAGCATATAATCTTAACTGAGGCTCATAAAGCTTGTTTGAAATAAGGGTCG 1380 5630 [

Qy 2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAA.	Qy 2341 GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAA 	SULT 8 356454 10/c 1tinuation (11 of 22) o	into 22 fragments LoCUS ABS56454 nme Begin End 1 110000 100001 210000	ABS56454 02 200001 ABS56454-03 300001 ABS56454 04 400001 ABS56454-05 500001	MP ABS56454 06 60001 710000  WP ABS56454 08 800001 910000  WP ABS56454 09 900001 1010000	ABS56454 10 1000001 ABS56454 11 1100001 ABS56454 12 1200001 ABS56454 13 1300001	ABS56454 14 1400001 ABS56454-15 1500001 ABS56454-16 1600001 ABS56454-17 1700001	ABS56454 18 1800001 ABS56454 19 1900001 ABS56454 20 2000001 ABS56454 21 2100001	Query Match 97.9%; Score 2338; DB 7; Len Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; In	OY 1 TICTTAGGAGTIGGGACTGTATCAAGGTAGAAGGATAAGGAA	Qy 61 TATAGATGGAAAACAAGCGACGAAAAACGGAGAATTTGACT	Oy 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAGATAACA	Qy 181 TTCACATGGCGACCACTATCATTACTATGGTAAGGTTCCT	OY 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGAT	Qy 301 GGTCAAGGGTGGATATGTTATCAAGGTAGAAATACTAT 	Qy 361 IGCCCACGCGGATBACGTCCGTACBAAAQAGGAAATCAATCGA 	Qy 421 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGCTGCTGTTT 	
1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGG 1260 105750 GAAAGATTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGA 105691	1261 TGTTTCACACTCTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 	1321 TGATAAAGCATATAATCTGTDAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380 	1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGATGACTGATT 1440 	1441 TAAACAAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG 1500 	1501 ACTICGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT 1560 	1561 AGCTGATAACTATACAACGTCAGATGGTTACATTTTTGATGAACATGATAATCAGTGA 1620 	1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG 1680 	1681 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740 	1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800 	1801 CAATCGTGAAAGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 1860 	1861 TACAGTIGAGGITAAAAACGGTAAITIGAITAITCCTCATAAGGATCAITACCATAAIAI 1920 	1921 TAAATTTGCTTGGTTTGATCACACATACAAAGCTCCAAATGGCTATACCTTGGAAGA 1980 	1981 TITGTIGCGACGATTAGTACTACGTAGAACACCCTGACGAACGTCCACATICTAATGA 2040 	2041 TGGATGGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA	2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160 	2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGAAGATTTTGCTTGC	2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGTTTACGAAATAA 2280 	
Qy Db	oy da	Å A	QY Db	S G	QV Db	QV Db	oy do	ζς Q	ąg V	ζς qq	Qy DP	S Pa	δ, dg	P G	Vy qa	Qy Pp	ζς 40	

(Streptococcus pneumoniae type 4 st SAAGCAGAAAATTACTTGC 2340 0 AAAATAATCGTGTTTCCTA 60 CAGACCAAGGCTATGTCAC 180 CTTATGACGCTATCATCAG 240 ATGAGGATATTGTTAATGA 300 ATGITIACCITAAGGAIGC 360 Indels 0; Gaps AAAATAAAC 2389 |||||||||| AAAATAAAC 104562 ength 110000; 6

106890 TATAGATGGAAAACAGCACCAAAAAACGCAGAATTTGACTCCTGATGAGGTTAGCAA 106831 121 GCGTGAAGGAATCATCCTGAGCAAATCGTCATCAACAAAACAGACTAACACCAAGGCTATGTCAC 180 106830 GCGTGAAGGAATCATGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180 106710 TTCACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTATGTCAC 106771 181 TTCACATGGCGACCACTATCATTACAATGGTCAGATCCTTATGACGCTATCATCAC 240 106710 TTCACATGGCGACCACTATCATTAATAAAGGTTCCTTATGACGCTATCATCAG 106711 241 TGAAGAATTACTCATGAAAGATCCAAACTATAAGGCTAAAGAATAATGA 106711 106710 TGAAGAATTACTCATGAAAGATCCAAACTATAAGGCTAAAGAATTGTTAATGA 10651 106710 TGAAGAATTACTCATGAAAGATCCAAAAAGATGATAATGTTAATGA 106651 301 GGTCAACGTGGAAAACTATAAGAAAAAAAAAAAAAAAAA	106650   GTICHI	7 9 7	601 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 660 106350 ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA 106291 661 TTCAAGAACCTATCGCTGCAGAAATAGCGATAACACTTCAGAAACTGGGTACCTTC 720 106290 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAGACTAGCTTC 106231 721 TGTAAGCAATCGAGAACTACAATAGTAACACAGGAACAACAGGAACACTAACAGTTC 106231 106230 TGTAAGCAATCCAGGAACTACAATAGTAACACAAGCAACACACAAAACAGCAACACACAACAGTCA 106171 106230 AGGAAGTCAAAGTAATGATAGTAATGATAAAACAGCACAAAACTGCCTTTCAG 840	106170   AGCAAGTCAAAGAATTGATTGATTGTTTGATACCAACACAAATCCAAAATTGATGATTGAT	1021 GGTACCAGATTCAAGGCCAGAACAACTCCAACCGACTCCGGAACCTAGTCCAGG 1080 105930 GGTACCAGATTCAAGGCCAGAACCAACCAACTCCACACCGGAACCTAGTCCAGG 10801 1081 CCCGCAACCTGCACCAAATCTTAAAATAGACTCCAAATTCTTTTGGTTAGTCAGCTCGG 105871 105870 CCCGCAACCTGCACCAAATTTAAAATAGACTCAAATTCTTTTTTTT
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Db 4913 TACAGTTGAGGTTAAAAACGGTAATTGATTATTCCTCATAAGGATCATTACCATAATAT 4972  Qy 1921 TAAATTTGCTTGGTTTGATGATCACATACTCCTCAAATGGCTATACCTTGGAAGA 1980  Db 4973 TAAATTTGCTTGGTTTGACACACATACACACCCTGACGAATGGCTATACCTTGGAAGA 5032  Qy 1981 TTTGTTTGCGACGATTAAGTACTACGTAGAAACCCCTGACGAACGTCCACATTCTAATGA 2040  Db 5033 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 5092  Qy 2041 TGGATGGGGCAATGCCAGTGAGCATGTTAAGACAGAAAAGACCACAGGAAGATCCAAA 5152  Qy 2101 TAAGAACTTCAAAGCGGATGATGATGATTAAGGCAAAAAAAA	153 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTTCTGCTTGCT		22) of ABS56456 nto 22 fragment e Begin 1 10001 200001 300001 600001	ABSS6454_07 ABSS6454_08 ABSS6454_09 ABSS6454_10 ABSS6454_10 ABSS6454_11 ABSS6454_11 ABSS6454_11 ABSS6454_13 ABSS6454_14 ABSS6454_15 ABSS6454_15 ABSS6454_15 ABSS6454_16 ABSS6454_17 ABSS6454_17 ABSS6454_17 ABSS6454_17 ABSS6454_17 ABSS6454_17 ABSS6454_17 ABSS6454_19 ABSS6454_20 ABSS64	ABSS6454_Z1 Z100001 Z16259  Query Match Best Local Similarity 100.0%; Pred. Matches 2388; Conservative 0; Mism 1 TTCTTACGAGTTGGGACTGTATCAAGC 106950 TTCTTACGAGTTGGGACTGTATCAAGC 1106950 TTCTTACGAGTTGGGACTGTATCAAGC 110691 TTATAGATGGAAAACAAGCGAAAAAGTGAAGAAAAGTGAAGAAAAAGAAGGAAG

probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 191, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is phomologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified system for identifying fragments of the S. pneumoniae genome of system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae 

Sequence 8195 BP; 2688 A; 1622 C; 1777 G; 2105 T; 0 U; 3 Other;

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3232 ô 3112 3172 3292 3352 3412 3472 3532 3533 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 3592 3652 3712 TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC 3772 3832 120 240 180 300 360 420 480 540 900 099 720 780 AGCAAGTCAAAGTAATGACATTGATAGTCTTTGAAACAGCTCTACAAACTGCCTTTGAG 840 9 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTTCCTA TTCACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA 3353 GSTCAAGGGTGGATATGTTATCAAGGTAGAAAATACTATGTTTACCTTAAGGATGC 3473 TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 3413 recenegeserrancereceracaaaasasasaareaareaaaaaaaaaaaasaaas TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAACAACACAACAGTCA TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA **AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC** TTCAAGAACCTATCGCCGACAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAACAGGAACACTAACAGTCA TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT ATCAGCTAGCGAGTTGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA ; 0 Length 8195; Indels DB 2; 97.9%; Score 2338; Dilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Query Match Best Local Similarity Matches 2388; Conserv 3053 3113 121 3173 181 3293 541 3653 3713 61 3593 601 661 301 361 421 481 721 781

4012 1080 1140 1200 4312 4372 1380 1500 1560 4432 4492 4552 4672 4792 1920 TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCTTACTCTCAAAT GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCTCAAAT GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG ACGAAAAGTTGGGGAAGGATATTGAATTCGAAGAAAAGGCCATCTCTCGTTATGTCTTTTGC GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGAG TGTTTCACACACTTTAACTGCTAAAAAAAAAATGTTGCTCCTCGTGACCAAGAATTTTA **ACGADAAGTTGGGGAAGGATATGTATTCGAAGAAAAAGGGCATCTCCGTTATGTCTTTGC** TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG ACTTGGCAAACCAAATTCTCAAATTGAGTATACTGAAGACGAAGTTCGTATTGCTCAATT TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAAGATAG CCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAAGGTATCCTACC CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAGGTATCCTACC TACAGTIGAGGITAAAAACGGTAAITIGAITATICCICAIAAGGAICAITACCAIAATAI 4433 TAATICIGATITCCAAGCCITAGACAATIATIAGAACGCTIGAAIGAIGAACGACTAA 4493 TAAAGAAAATTGGTAGATGATTTATTGGCATTCCTAGCACCAATTACCCATCCAGAGCG ACTIGGCAAACCAAATICICAAATIGAGIATACIGAAGACGAAGIICGIATIGCICAAII AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA CAATCGTGTGAAAAGGGGAAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA CAATCGTGTGAAAGGGGAAAACGAATTCCACTCGTTCGACTTCCATATATGGTTGAGCA 3953 4073 4133 4373 ' 961 4013 1081 1141 4193 1201 841 901 1021 1261 4313 1381 4253 1321 1501 4553 1561 4613 1621 4673 1681 4733 1741 4793 1801 4853 1861 1441 셤 g ò ð 8 ద ò d 8 8 ò qq 임 ò g à  $\delta$ 임 d ద ð à ò g ò Dp ठ 셤 ð g ò 엄 à g à

	RESULT 6 AAV52227  ID AAV52227  ID AAV52227  XX AC AAV52227; XX DT 23-OCT-1998 (first entry) XX DE Streptococcus pneumoniae genome fragment SEQ ID NO:94. XX	HUMA-) HUMAN GENOME SCI INC.  XX  Kunsch (CA, Choi GH, Dillon PJ, Rosen CA, Barash SC, Fannon M;  PI Dougherty BA;  XX  WPI; 1998-272225/24.  XX  Computer-readable medium with recorded Streptococcus pneumoniae  PT Computer-readable medium with recorded Streptococcus pneumoniae.  PT Pharmaceutical compositions and vaccines for Streptococcus pneumoniae.  XX  Claim 1; Page 727-732; 1409pp; English.  XX  The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical componity or 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences from Streptococcus con it, or a represent invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments from Streptococcus concented encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a
901 AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCAAAT 960 918 AGCTAGAGGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCTCTCAAAT 977 961 GTGTGAATTGCAGAACGAACGAATCATTACCACTTCATCCTCTCAAAT 977 978 GTCTGAATTGCAACGAACGAACGAATCATTATCCCCTTCGTTACACGTTG 1020 978 GTCTGAATTGGAAACGAACGAACGAATTATTCCCCTTCGTTACACGTTG 1037 1038 GGTACCAGATTCAAGGCCAGAACACCCAAGTCCACACCCCTTCGTTACACCATTG 1037 1041 GGTACCAGATTCAAGGCCAGAACAACTCCACAACCGACTCCGGAACCTAGTCCAGG 1080 1051 GGTACCAGATTCAAGGCCAGAACAACTCCACAACCGACTCCGGAACCTAGTCCAGG 1097 1061 CCCGCAACCTGCAAACAACAACTCCACAACCCACACCGCAACCTAGTCCAGG 1097 1061 CCCGCAACCTGCAAATTAAAATAGATCCACAAATTCTTTTGGTTAGTCATTGCTTTGC 1200 11141 ACGAAAAGTTGGGGAACGATATGTATTCGAAAATTCTTTTTTTGGTTAGTCTTTGC 1207 1158 ACGAAAAGTTGGGGAACGATATGTATTCGAAAAAAAAGGGCATCTCTCTTTTGGTTATGTCTTTGC 1207 1158 ACGAAAAGTTGGGAAATTCGAAAAAAAAAAAAAAAAAAA		1 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAGAAAAGGTATCCTACC 1 CCTTTCTGATAAGGAAAAGTTGCAGCTCAAGCCTATACTAAAAAAAA

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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2469 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence. The first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having the complement of the target sequence to the complement of the complement of the carget sequence to the complement of the carget sequence to the complement of the carget sequence to the carget sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying
                                             TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAATTACTTGC
TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGGGAGAAAATTACTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene, ds; bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                   GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAATAAAC 2389
                                                                                                                                                                       GTTGTTAAAAGGAAGTAATCCTTCATCTGTAAGTAAGGAAAAATAAAC 2448

 S. pneumoniae type 4 strain coding region #1174.

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INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                   ABX06886 standard;
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                identified coding region from the genomic sequence. Note: The sequence data for this parent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at the part ftp.wipo.int/pub/published_pct_sequences. (Updated on 27-OCT-2003 to
                                                                                                                                                                                                                                                 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAAGGAAAATAATCGTGTTTCCTA
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immunodominant proteins. The present sequence is one of the 2489
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                                                                                                                                                          Length 2406;
                                                                                                                         Sequence 2406 BP; 834 A; 461 C; 490 G; 621 T; 0 U; 0 Other;
                                                                                                                                                                                           1; Indels
                                                                                                                                                        Query Match

97.9%; Score 2338; DB

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2388; Conservative 0; Mismatches
                                                                                    standardise OS field)
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Although a number of proteins have been suggested as being involved in the pathogenicity of Streptococcus pneumoniae, there still remains a need to identify polypetides having epitopes in common from various strains of S. pneumoniae in order to utilise such polypeptides in vaccines to protect against a wide variety of S. pneumoniae. New vaccine compositions are described which comprise a Streptococcus pneumoniae polypeptide (or fragments) of 80 - 680 amino acids in length that comprise at least one histidine triad residue (HaxAHAI) or a coiled-coil region, or an antibody adainst these features. The vaccine is useful in protecting against infection by Streptococcus pneumoniae. The vaccine composition comprising antibodies to is useful for passive immunization for treating Pneumococcal infections which includes otitis media, nasopharyngeal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine useful for prophylaxis and treatment of pnemococcal infections such as otitis media, nasopharyngeal and bronchial infections, comprises Streptococcus pneumoniae proteins.
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                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; infection; vaccine; colled coil region; histidine triad residue; 8785; antibody; otitis media; nasopharyngeal infection; bronchial infection; bronchitis; sepsis, meningitis; lobar pneumonia; ds.
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Sequence 2451 BP; 849 A; 467 C; 499 G; 635 T; 0 U; 1 Other;
                                                                                                                                                                                                                                      S. pneumoniae
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ive 0; Mismatches
                                                                                                                                                                                                                                      (Sp36A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotide encoding Streptococcus pneumoniae polypeptides useful for producing vaccines for prevention or attenuation of infection by Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                      Antigen; ds; bacterial infection; vaccine; pneumonia; antibacterial.
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100.0%; Pred. No. 0;
tive 0; Mismatches
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97US-00961083.
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P-PSDB; ADC45137.
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nes 2389; Conserv
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Oy 2341 GTTGTTAAAA                   Db 2341 GTTGTTAAAA	RESULT 2 ABQ84819 ID ABQ84819 standard; XX AC ABQ84819; XX. DT 04-SEP-2002 (first	XX DE S. pneumoniae SP036 XX XX KW Streptcocccus pneum			30-OCT-1997;	PA (KUNS/) KUNSCH C A. PA (BARA/) BARASH S C. PA (DILL/) DILLON P J. PA (DOUGHERTY B	(FANN/) (ROSE/) Choi GH	Rosen CA; WPI; 2002-479261/ P-PSDB; ABP54584.		_	CC Abba4/92 to Abba499 CC Streptococcus pneum CC pneumoniae antigens CC vaccines. The S. pr		Seque	Query Match Best Local Similarity Matches 2389; Conser	Oy 1 TICTTACGAC	61	61	I QY 121 GCGTGAAGG
1261 IGTTTCACACTTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 1261 IGTTTCACACCTTTAACTGCTAAAAAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320	1321 TGATAAAGCATATAATCTGATAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380 1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAAATAAGGGTCG 1380 1381 TAATTCTGATTCCAAGCCTTAGACAAATTATAGAACGCTTGAATGAA		1501 ACTIGGCAAACCAAATICICAAATIGAGTATACIGAAGACGAAGTICGTATIGCTCAATT 1560 	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATAAATCAGTGA 1620 	1621 TGAAGGAGATGCATATGTAACGCCTCATATGGGCCATAGTCACTGGATTGGAAAGATAG 1680 	1681 CCTTTCTGATAAGGAAAAAGTTGCAGGTCAAGCCTATACTAAAGAAAAAGGTATCCTACC 1740 	1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCAGTTTA 1800 	1801 CARICGIGIGAAAGGGAAAAACGAAITCCACTGCITCGACITCCAIAIAIGGIIGAGCA 1860 	1861 TACAGTIGAGGITAAAAACGGTAAITIGAITAITCCICAIAAGGAICAITACCAIAAIAI 1920 	1921 TAAAITITGCITGGITTGAIGATCACACATACAAAGCTCCAAAIGGCIATACCITGGAAGA 1980 1921 TAAAITIGCITGGITTGAIGACACATACAAAGCTCCAAAIGGCIAIACCTIGGAAGA 1980	1981 TITGTITGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAAIGA 2040 1981 TITGTITGCGACGATTAAGTACTACGTAGAACACCCTGACGAAGAACGTCCACATTCTAAIGA 2040	2041 TGGATGGGGCAATGCCAGTGATGTGTTAGGCAAGAAAGACCACAGTGAAGATCAAA 2100 	2101 TAAGAACTTCAAAGCGGATGAAGAGCCAGTAGAGGAAACACCTGCTGAGCCAGAAGTCCC 2160	TCAAGAACTICAAAGCGGAATGAAGAGCCGAAGTGAAGAAGAAGCGGGGGGGG	2161 TCAAGTAGAGACTGAAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAAJTTTGCUAAA 2220 2221 AGTAAGGGATTCTAGTGTAAAGCGAATGGAACAGAAAAGCTGGTTGGT		2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGGAGAAAATTACTTGC 2340 	

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unoniae antigens given in ABP54557 to ABP54669. The S. moniae antigens given in ABP54557 to ABP54669. The S. mis have antibacterial activity and can be used in preumoniae antigens can also be used to prevent or tococcal infection in an animal. The polynucleotides menuoniae antigens can be used to detect Streptococcus (ORF84005 to ABQ85130 represent primers used in the cloning ORF8 (open reading frames) which are used in an example invention
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100.0%; Score 2389; DB 6; Length 2389; y 100.0%; Pred. No. 0; rvative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                         moniae; epitope; vaccine; antigenic protein; eptococcal infection; detection; gene; ds.
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961 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020
           121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180
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                                                               TTCACATGGCGACCACTATCATTATTACAATGGTAAGGTTCCTTATGACGCTATCATCAG
                                                                                                              181 Trcacargecgaccacrarcarrarracaargeraagerrecrrargacgerarcarcag
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or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a protein from Streptococcus pneumoniae. The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
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                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
7. 2389
/*tag= "SP036"
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/fransl_except= (pos:1367. .1369,aa:Xaa)
/note= "no stop codon given; Xaa is unspecified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding antigenic peptide(s) from Streptococcus - or their epitope-containing fragments, useful in protective therapeutic vaccines, and for diagnosis.
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2 (b. ) Choi, G.H., Johnson, S.L. and Hromockyj, A.

2 (b. ) Choi, G.H., Johnson, S.L. and Hromockyj, A.

3 (b. ) Choisostis antigens and vaccines

3 (b. ) Choisostis A 33 24-APR-2001;

4 (b. ) Human Genome Sciences INC

4 (b. ) D 24-APR-2001

5 (b. ) D 24-APR-2001

6 (b. ) D 24-APR-2001

6 (b. ) D 24-APR-2001

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7 (c. ) D 24-APR-2001

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Streptococcus pneumoniae antigens and vaccines.
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SNAKETLTGLKNNLLPGTQDNNTIMAEAEKLLALLKESK"
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Choi.G.H., Kunsch,C.A., Barash,S.C., Dillon,P.J., Dougherty,B.,
Fannon,M.R. and Rosen,C.A.
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100.0%; Pred. No. 2.2e-16;
tive 0; Mismatches 0; Indels
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7, 2.2e-16;
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1 (Dasses 1 to 2290)
Choi, G.H., Kunsch, C.A., Barash, S.C., Dillon, P.J., Sannon, M.R. and Rosen, C.A.
Streptococcus pneumoniae antigens and vaccines Patent: US 6573082-A 65 03-JUN-2003;
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tive 0; Mismatches
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/mol_type="unassigned DNA"
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Sequence 65 from patent US 6573082.
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US 6159469.
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/organism="unknown"
/mol_type="genomic DNA"
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A61P29/00,
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A61P37/04,A61P37/06,A61P43/00,C07K16/40,C12N1/15,C12N1/19, PC
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PC C12N5/10,C12N9/48,C12P21/08,C12N15/00,C12N5/00,A61K37/02 CC
Human complement C3-degrading polypeptides from streptococcus CC
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PN 4P 2002526082-A/1
PD 20-AUG-20002
PP 24-SEP-1999 JP 2000574269
PR 24-SEP-1998 US 60/101736,31-MAR-1999 US 09/283094 PI
MARGARET K HOSTETTER, DAVID J FINKEL, QI CHENG, BRUCE A GREEN,AMY
                                                                                                                                                    [ Jases 1 to 504]

Hostetter, M.K., Finkel, D.J., Cheng, Q., Green, B.A. and Masi, A.W. Human complement C3-degrading polypeptides from streptococcus Patent: JP 2002538082-A 1 20-AUG-2002;
REGENTS OF THE UNIVERSITY OF MINNESOTA, AMERICAN CYANAMID CO
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Hostetter, M. K., Finkel, D.J., Cheng, O., Green, B.A. and Masi, A.W.
Hostetter, M. K., Finkel, D.J., Cheng, O., Green, B.A. and Masi, A.W.
Human complement C3-degrading polypeptides from streptococcus
Parent: JP 2002526082-A 2 20-AUG-2002;
Streptococcus pneumoniae
PD 20-AUG-2002
PD 20-AUG-2002
PP 24-SEP-1999 JP 2000574269
PR 24-SEP-1999 US 60/101736,31-MAR-1999 US 09/283094 PI
MARGARET K HOSTETTER, DAVID J FINKEL, QI CHENG, BRUCE A GREEN, AMY
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PC C12N5/10,C12N9/48,C12P21/08,C12N15/00,C12N5/00,A61K37/02 PC C12N5/10,C12N5/00,A61K37/02 PC C12N5/10,C12N5/00,A61K37/02 PC C12N5/10,C12N5/00,A61K37/02 PC C12N5/10,C12N5/10,C12N5/10,C12N5/00,A61K37/02 PC C12N5/10,C12N5/10,C12N5/00,C12N5/00,A61K37/02 PC C12N5/00,C12N5/00,C12N5/00,A61K37/02 PC C12N5/00,C12N5/00,C12N5/00,A61K37/02 PC C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C12N5/00,C
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Human complement C3-degrading polypeptides from streptococcus
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   JP 2002526082-A/1.
Streptococcus pneumoniae
Streptococcus pneumoniae
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/mol_type="genomic DNA"
/db_xref="taxon:1313"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 53; DB 100.0%; Pred. No. 2.4 tive 0; Mismatches
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Streptococcus pneumoniae
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JP 2002526082-A/2.
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                                                                                                                                Streptococcus.
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Best Local Similarity
Matches 53; Conserv
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1 (bases 1 to 2166)
Zhang,Y., Masi,A.W., Barniak,V., Mountzouros,K., Hostetter,M.K. and
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/protein_id="AAX2630.1"
/db_xref="d1:1347096"
/translation="MKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKDAAHADNIRT
KEEIKRQKQEHSHNHGGGSNDQAVVAARAQGRYTTDDGYIFNASDIIEDTGDAXIVPH
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YEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPSPQPADNPQPAPSNP
IDEKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAK
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DILAFLAPIRHPERLGKPNAQITYTDDEIQYAKLAGKYTTEDGYIFDPRDITSDBGDA
YVTPHWITSHWIKKUSLSBRRAAAQXYAKEKGLIFPSTDHQDSGWTEAKGAEAIYNR
VKAAKKVPLDRMPYYLQYIYGVKNGSLIIPHYDHYHNIKFBWFDEGIYBARGAEAIYNR
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USA
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Zhang,Y., Masi,A., Barniak,V., Mountzouros,K., Hostetter,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant PhpA protein, a unique histidine motif-containing protein from Streptococcus pneumoniae, protects mice against intranasal pneumococcal challenge intransal pneumococcal challenge infect. Immun. 69 (6), 3827-3836 (2001)
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/note="N-terminal truncated PhpA protein; histidine
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="derived from Streptococcus pneumoniae PhpA
                                                                                organism='Streptococcus pneumoniae'
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Submitted (25-JAN-2001) Department of Bacteriology, W
Vaccines, 211 Balley Road, West Henrietta, NY 14586,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Length 504;

    .504
/organ="Streptococcus pneumoniae"
/mol_type="genomic DNA"
/db_xref="taxon:1313"

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                             Location/Qualifiers
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выддууу о 504 bp DNA linear PAT 17-JUL-2003
Human complement C3-degrading polypeptides from streptococcus
pneumoniae.
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Patent: WO 0198334-A 4 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
Location/Qualifiers
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100.0%; Pred. No. 1.1e-67;
Live 0; Mismatches 0; Indels (
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                                                                                                                                                               0; Indels
       /organism='S. pneumoniae'
                                                                                                                                 6.2%; Score 148; DB 6; I ilarity 100.0%; Pred. No. 1.1e-67; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="BVH-11"
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                                            1. ,2647
/organism="unidentified"
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1. ,2647
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BD229970.1 GI:33039740
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JP 2002533123-A/7
08-OCT-2002
20-DBC-1999 JP 2000591190
23-DEC-1999 US 60/113800
23-DEC-1998 US 60/113800
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C12N15/09,A61K39/00,A61K39/09,A61K39/39,A61P11/00,A61P25/00,
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Hamel, J., Brodeur, B.R., Pineau, I., Martin, D., Rioux, C. and
Charland, N.
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Key Location/Qualifiers
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Patent: JP 2002533123-A 7 08-OCT-2002;
SHIRE BIOCHEM INC
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/noFe="BVH-11"
                                                                                                                                                                                                                  Streptococcus antigens
Patent: WO 0198334-A 3 27-DEC-2001;
SHIRE BIOCHEM INC. (CA)
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                                                            AX343072 2523 bp
Sequence 3 from Patent WO0198334.
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JP 2002533123-A/7.
unidentified
unidentified
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DEFINITION
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826 AACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTAC 885
                                                                                                                    707 AACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAAGC
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                                                                                                                                                          766 AACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAATACTAAACAACAAGAACAAGA
                                                                                                                                                                                               767 AACACTAACAGTCAAGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTAC
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Hamel,J., Brodeur,B.R., Pineau,I., Martin,D., Rioux,C. and
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Patent: JP 2002533123-A 2 08-OCT-2002;
SHIRE BIOCHEM INC
OS S. Dneumoniae
PN JP 2002533123-A/2
PD 08-OCT-2002
PP 20-DEC-1999 JP 2000591190
PR 23-DEC-1999 US 60/113800
PR JOSEE HAMEL, BERNARD R BRODEUR, ISABEI
        Mismatches
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Streptococcus.

1 (bases 1 to 2535)

Zhang,Y., Masi,A.W., Barniak,V., Mountzouros,K., Hostetter,M.K. and Green,B.A.

Recombinant PhpA protein, a unique histidine motif-containing protein from Streptococcus pneumoniae, protects mice against intranasal pneumococcal challenge

Infect. Immun. 69 (6), 3827-3836 (2001)
                                                                                                                                                                                                                                                                            ar340221
Streptococcus pneumoniae PhpA (phpA) gene, complete cds.
AF340221
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QATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEE
LLMKDPNYQLKDEDIISEIKGGYVIKVDGKYYYYLKDAAHADNVRTKEEINRQKQEHS
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ELSASELAAAKAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSYGNNPGTTNTNTSRNSN
TNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQIISRTANGVAVPHGDHYHF
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NPIDEKLYKEAVRKYGDGYVPEENGYPRYIPAKDLSAETAAGIDSKLAKQESLEHKLG
AKKTDLPSSPREFYNKAYDLLARIHQDLLDNKGRQYDFEALDNLLERLKDVSSDKYKL
VDDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDPRDITSDEG
                                                                       DAYVTPHMTHSHWIKKDSLSEAÈRAAQAYAKEKGLTPPSTDHODSGNTEAKGAEAIY
NRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGYSL
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EETPREEKPQSEKPESPKPTEEPEEESPEESPEESEEPQVETEKVKEKLREAEDLLGK
    745
                                        527
                                                                                                 Direct Submission
Submitted (25-JAN-2001) Department of Bacteriology, Wyeth Lederle
Vaccines, 211 Bailey Road, West Henrietta, NY 14586, USA
Location/Qualifiers
AGCGATAACACTTCAAGAACAAACTGGGTACCTTCTGTAAGCAATCCAGGAACTACAAAT
                        2 (bases 1 to 2535)
Zhang,Y., Masi,A., Barniak,V., Mountzouros,K., Hostetter,M. and
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/note="histidine motif-containing protein"
                                                                                                                                                                           806 AGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAGTCAACG 846
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/mol_type="genomic DNA"
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/product="PhpA"
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08-077-2002
20-DEC-1999 JP 2000591190
23-DEC-1999 US 60/113800
UOSEE HAMEL, BERNARD R BRODEUR, ISABELLE PINEAU, DENIS MARTIN, PI
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Coding region of BVH-11 gene
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Length 2535;

8.4%; Score 200; DB 1; I 100.0%; Pred. No. 9.3e-96;

Query Match Best Local Similarity

ORIGIN

SPNEU1929 LOCUS LOCUS LOCUS DEFINITION Streptococcus pneumoniae clone ACCESSION AL49951 VERSION AL49951 AL4995	TITLE Annotated draft genomic sequer type 19F clinical isolate JOURNAL Microb. Drug Resist. 7 (2), 95 WEDLINE 2135329 PUBMED 11442348 REFERENCE 2 (bases 1 to 702) AUTHORS Dopaco, J., Mendoza, A., Herrerc	TITLE Direct Submission  TITLE Direct Submission  JOURNAL Submitted (31-OCT-2000) Reseauseron  COMMENT * NOTE: This is a 'working dra' This sequence will be replaced to the sequence of the s	* the introduce as * the accession number will be Location/Qualifiers 1. 702 1. 702 /organism="Streptocoon" /mol. type="genomic Diagon" /db.xref="teaxon:1313"	ORIGIN  Query Match  Best Local Similarity 99.1%; Pred. Natches 576; Conservative 0; Mism	Qy 266 AACTATAAGCTAAAAGATGAGGATATTY	Db 108 GTAGATGGAAATACTATGTTTACCTT  Qy 386 AAAGAGAAATCAATCGACAAAACAA  DD 168 AAAGAGGAAATCAATCGACAAAAAAAAAAAAAAAAAAAA		Oy 566 GAGATCATTACCATTACATTCCTAAG  Db 348 GAGATCATTACCATTACATTCCTAAG  OY 626 GAAGATCATTACCATTACATTCCTAAG  OY 626 GAAGCCTTCCTATCTGGTCGAGAAAT  Db 408 GAAGCCTTCCTATCTGGTCGAGGAAAT
	18613 AGTTCGTATTGCTCAATTAGCTGATAAGTATACAACGTCAGATGGTTACATTTTGATGA 18672  1603 ACATGATAAATCAGTGATGAAGGAATGCATATGTAACGCTCATATGGGCCATAGTCA 1662  18673 ACATGATATAATCAGTGATGAAGGAATGCATATGTAAGCCCTCATATGGGCCATAGTCA 18732  1663 CTGGATTGGAAAAGATAGCTTTTCTGATAAGGAAAAGTTGCAGCTCAAGCTATACTAA 1722  18733 CTGGATTGGAAAAGATAGCTTTCTGATAAGGAAAAAGTTGCAGCTCAAGCTATACTAA 18792	1723   AGAAAAAGGTATCCTACCTCCATCTCCAGACGCAGATGTTAAAGGAAATCCAAATGGAGA   1782		1963 IGGCTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGAACGA 2022 19033 IGGCTATACCTTGGAAGATTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGA 19092 2023 AGGTCCACATTCTAGAAGAGATTGGTTGCGATGCCAGTGAGCATGTTTAGGCAAGAAAGA	19093 AGTCCACATTCTAATGATGGATGGGCAATGCCAGTGAGCATGTGTTAGGCAAGAAAGA	a recrease and the contrared and a contrared a	AGAGGTTTTGCTTGCGAAAGTAACGGATTCTAGTCTGAAAGCCAATGCAACGGAAACTCT AGCTGGTTTACGAATAATTTGACTTTCAATTATGGATAACAATAGTATCTGGCAGA AGCTGGTTTACGAATAATTTGACTTTCAAATTATGGATAACAATAGTATCATGGCAGA AGCTGGTTTACGAAATAATTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGA	2323 AGCAGAAAATTACTTGCGTTGTTAAAAGAAATCATCTCATCTTGAGTAAAGAAAA 2382 19393 AGCAGAAAAATTACTTGCGTTGTTAAAAGAAATCCTTCATCTGTAAGTAA
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RESULT 14

ro,J., Caldara,F., Polissi,A., rier,M., Grand-Schenk,E., Gandin,C., de r,G., Garcia,E., Peitsch,M. and 0 ATCTGTCAAATTCAAGAACCTATCGCCGACAAAAT 685 bp DNA linear HTG 11-JUL-2001 ne G54, \*\*\* SEQUENCING IN PROGRESS \*\*\*. ro,J., Caldara,F., Humbert,Y., nd-Schenk,B., Gandin,C., de ell,G., Feger,G., Garcia,B., Peitsch,M. TAAGGATGCTGCCCACGCGATAACGTCCGTACA 385 AGAATGAGTTATCAGCTAGCGAGTTGGCTGCTGCA 625 TGTTAATGAGGTCAAGGGTGGATATGTTATCAAG 325 AGGAGATAGTCAACATCGTGAAGGTGGAACTCCA 445 ACGTTCGCAAGGACGCTATACTACAGATGATGGT 505 AGAGGATACTGGTGATGCTTATATCGTTCCTCAT 565 warch Department, Glaxo Wellcome, S.A., antos, SPAIN Iraft' sequence. ence from a Streptococcus pneumoniae 0; Gaps us soon as it is available and be preserved. acillales; Streptococcaceae; 326; DB 2; Length 702; No. 9.7e-164; smatches 5; Indels coccus pneumoniae" DNA" 99-125 (2001) 3.

Dopazo, J., Mendoza, A., Herrero, J., Caldara, F., Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C., de Francesco, M., Polissi, A., Buell, G., Feger, G., Garcia, E., Peitsch, M. and Garcia-Bustos, J.F.
Annotated draft genomic sequence from a Streptococcus pneumoniae type 19F clinical isolate
Microb. Drug Resist. 7 (2), 99-125 (2001)

(bases 1 to 20035)

21335329 11442348

Streptococcus pneumoniae Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,

Streptococcus pneumoniae

Streptococcus.

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S.A.,

Jopazo, J., Mendoza, A., Herrero, J., Caldara, F., Polissi, A.,
Humbert, Y., Friedli, L., Guerrier, M., Grand-Schenk, E., Gandin, C.,
Francesco, M. Buell, G., Feger, G., Garcia, E., Peitsch, M. and
Garcia-Bustos, J.F.

Direct Submission
Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A.
Severo Ochoa 2, 28760 Tres Cantos, SPAIN
\* NOTE: This is a "working draft' sequence.
\* This sequence will be replaced
\* by the finished sequence as soon as it is available and
\* the accession number will be preserved.

/organism="Streptococcus pneumoniae"

Location/Qualifiers

/mol\_type="genomic DNA" /serotype="genomic DNA" /db\_xref="taxon:1313" /clone="G54"

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SOURCE
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17953 CAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACAGGAGATCATTACCACTTC 18012 18072 18192 18372 1003 1063 1183 1243 943 CAAATCACAAGTCGAACAGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTC ATCCCTTACTCTCAAATGTCTGAAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGT COGGAACCTAGTCCAGGCCCGCAACCTGCACCAAATCTTAAAATAGACTCAAATTCTTCT TTGGTTAGTCAGCTGGTACGAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATC 1184 ICICGITAIGICITITGCGAAAGAITIACCAICIGAAACIGIIAAAAAICTIGAAAGCAAG 18373 CGTGACCAAGAATTTTWTGATAAAGCATATAATCTGTTAAACTGAGGCTCATAAASCCTTG TTTGNAAATAAGGGTCGTAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTG CGTGACCAAGAATTTTATGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTG Length 20035; 9; Indels DB 2; 38.8%; Score 927; DB 99.3%; Pred. No. 0; ive 0; Mismatches Query Match 38.8 Best Local Similarity 99.3 Matches 1497; Conservative 944 884 1004 1064 1124 1244 1304 18253 18313 1364 QQ ò g ð

Streptococcus pneumoniae clone G54, \*\*\* SEQUENCING IN PROGRESS \*\*\*. AL449937.1 GI:11545162

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I LAVNGITGEVU INPUDEQAAE FRAAGERYSAKOKABRALLKDAQIVTADGKHFELAAN 
I GTPKDVEGVINNIGAEAVGLYRTEFIXMOSODFPTEDEOKYRSYNATLEGKNOKPVVR 
MPDIGGORELEYE FOMPHERMYNPEGFRAALRISISETGDAMFRTQIRALLRASVHGGLRI 
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DFFSIGTNDLI OYTMAADRMNEQVSYLYOPYNPSILELINNVI KAAHABGKWAGMCGE 
MAGDOQAVPLL VGMGLDEFSMSATSVLRTRSLMKKLDTAKMEBYANMELTEGSTMEBV
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                                    POPAPNIKIDSNSSLVSQLVRKVGEGYVFERKGISRYVFAKDIPSETVKNIESKLSKQ
ESVSHTITAKKENVARRDQEFYDKAYNILTEAHKALFENKGRNSDFQALDKILLERIND
ESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVATAQLADKYTTSDGYLIPE
BIJISDEGDAYTPHMGHSHWIGKDSLSDKEKYKAAQAYTKEKGILPPSPDADVKANPT
GDSAAJIYNRVKGEKIPLVRLPWHTVERVKNGNLIIPHKDHYNIKFAMPDHYY
KAPNGYTLEDILPATIKYYVEHPDERPHSNDGWGNASBHYLGKKDHSEDPHKNFKADEE
PVEETPAEPEVPQVETEKVEAQLKEAEVILAKVTDSSLKANATETLAGLRNNLTLQIM
DNNSIMAEAKILALLKGSNDS
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Pred. No. 0;
0; Mismatches
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complement(9861. .10124)
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Fri Oct

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PORDITUBDBOAYVTPHNTSHWIKNSSLSBERAAAQAYAREKGLIPPSTDHODSG
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GLYEAPKGYSLEDLLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNQQADTNOTEKP
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KLREAEDLIGKIQNPIIKSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKESK"
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PHGDHYHYIPKIBLSASELAAAERPLSGRGNLSNSRTYRRQNSDNTSRTNWVBSVSNP
GTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQIISRTAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KENNRUSY I DGKQATÖKTENLTPDEVSKREGI NAEQI VI KI TDQGYVTSHGDHYHYYN
GKVFYDAI FSEELLMKDPNYKLKDEDI VNEVRGGYV I KVDGKYYYYLKDAAHADNVRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Hypothetical protein"
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                                                                                                                                                                                                                                                                                                         product="Hypothetical protein"
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/rpt_unit="Rup A"
complement(2725. .5292)
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                                                    . .2081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2151. .2306)
/gene="spr1059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (2151. .2306)
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/note="synonym: s
complement(2725.
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                                                                                  BCT 13-SEP-2001
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FODFLEKNYLKTIWQVSKETPFSEMDFNMFKNISEKIIFERGSRALNDLKSNYXK"
                                                                       AE008479 13-SE.
Streptococcus pneumoniae R6 section 95 of 184 of the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome of the bacterium Streptococcus pneumoniae strain R6 J. Bacteriol. 183 (19), 5709-5717 (2001)
                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/strain="R6"
/db xref="taxon:171101"
complement(91. .738)
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/transl_table=11
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Streptococcus pneumoniae R6
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Db 5697 TGGATGGGCAATGCCAGTGACCATGTGTTAGGCAAGAAAGA	QY         2101 TAAGAACTTCAAAGCGGATGAAGACCAGTACAGAAACACCTGCTGAGCCAGAAGTCCC         2160           Db         5637 TAAGAACTTCAAAGCGGATGAAGACCAGTACAGGAAACACCTGCTGAGCCAGAAGTCCC         5578	OY 2161 TCAAGTAGAGACTGAAAAGTAGAAGCCCAACTCAAAGAAGCAGAAGTTTTGGTTGG	OY 2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAAGAAACTCTAGCTGGTTTACGAAATAA 2280  Db 5517 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAAACTCTAGCTGGTTTACGAAATAA 5458	OY 2281 TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCACAAAAATTACTTGC 2340  bb 5457 TITGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGCAGAAAAATTACTTGC 5398	Qy 2341 GITGITAAAAGGAACIAATCCTICATCIGTAAGGAAAAAAATAAC 2389 	ION NOI DS	SOURCE Streptococcus pneumoniae ORGANISM Streptococcus pneumoniae Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.	REFERENCE 1 AUTHORS Masignani, V., Tettelin, H. and Fraser, C. TITLE Streptococcus pneumoniae proteins and nucleic acids JOURNAL Patent: WO 02077021-A 4982 03-0CT-2002;	Chiron Spa (IT) ; THE INSTITUTE FOR GENOMIC RESEARCH (US)  FEATURES  Location/Qualifiers  Source  //Ordanism=Refrente/Coopers/Propers/	/mol_type="unassigned DNA" /db_xref="unassigned DNA" /db_xref="taxon:1313" /note="seq 4979 too long: 2.162.598 bases~replaced by	101.00 (101 to 0.100) (101 to 0.100) (101 to 0.149).980-seq 4980: from 0.300,001 to 0.649.980-seq 4981: from 0.600,001 to 0.949.980-seq 4981: from 1.500,001 to 1.549.980-seq 4984: from 1.500,001		Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2388; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	QY 1 TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA 60	OY 61 TATAGATGGAAACAAGCGACAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 120 	OY 121 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 180	QY         181         TTCACATGGCGACCACTATCATTACTAGGTAGGTTCCTTATGACGCTATCATCAG         240
961 GTCTGAATTGGAAGGAATCGCTGGTATTATTCCCCTTCGTTATCGTTCAACCATTG 1020 	CAGG	TGGT 11 	120	1201 GAAAGATTTACCATCTGAAACTGTTAAAAATCTTGAAAGCAAGTTATCAAAACAAGAGG 1260 	1261 TGTTTCACACACTTTAACTGCTAAAAAGAAAATGTTGCTCCTCGTGACCAAGAATTTTA 1320 	1381 TAAITCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGATTGACTAA 1440 	1441 TARAGAARATTGGTAGATGATTATTGGGATTCCTAGCACCAATTACCCATCCAGGGGG 1500 	1501 ACTIGGCAAACCAAAITCTCAAAIIGAGIAIACIGAAGACGAAGITCGIATIGCTCAAII 1560 	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620 			1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTA 1800 					5757 TTTGTTTGCGACGATTAAGTACTACGTAGAACACCCTGACGAACGTCCACATTCTAATGA 5698 2041 TGGATGGGGAATGCCAGTGAGCATGTTTAGGCAAGAAAGA

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                                                                                                                                  TTCTTACGAGTTGGGACTGTATCAAGCTAGAACGGTTAAGGAAAATAATCGTGTTTCCTA
                                                                                                      Gaps
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                                                                         1; Length 10256;
                                                                                                      Indels
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                                                                                                      Mismatches
                                                                           Score 2338;
Pred. No. 0
                                                                 97.9%; Scor
100.0%; Pre
                                                                               Query Match
Best Local Similarity 100.
Matches 2388; Conservative
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                AGCTAGAGGTGTTGCAGTGCCACACGGAGATCATTACCACTTCATCCCTTACTCTCTCAAAT
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                                                                                                                              TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC
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                                                              MICHAEL FANNON BRIAN A DOUGHERTY
C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,
                            CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, STEVEN C BARASH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3353 GGTCAAGGGTGGATATGTTATCAAGGTAGAAAATACTATGTTTACCTTAAGGATGC
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C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00,
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                                                                                                                                                                                                           /organism='Unidentified'
Location/Qualifiers
1. 8195
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2388; Conservative 0; Mismatches
 30-OCT-1997 JP 1998520718
31-OCT-1996 US 60/02998
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                                                                                                                                                Strandedness: Double;
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Key
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PC C12N1
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3533 AGGACGTATACTACAGATGATGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 3592  541 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 600  3593 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACCATTCCTAAGAATGAGTT 3652  601 ATCAGCTAGCGATTGCTGCTGCAGAAAATGGGAGAACTCGTGGAGAAATGAGTT 3652  602 ATCAGCTAGCAGATTGGCTGCTGCTGCTATCTGGTCGAGGAAATCGTCAAA  3653 ATCAGCTAGCAGATTGGCTGCTGCAGAAAATAGGGATAACATCTGTTCGTCAAAAATAGGATAACATCTGTCAAAAAAAA	TGTAAGCAATCCAGGAACTACAAATACTAACACAAGCAACAGCAACAGCAACAGTCA	AGCTAGAGGTGTTGCAGTGCCACGGAGATCATTACCACTTCATCCTTACTCTCTAAAT 960	1081 CCGCAACCTGCACCAATCTTAAATAGACTCAAATTCTTTTGGTTAGTCAGCTGGT 1140 4133 CCGCAACCTGCACCAATCTTAAATAGACTCAAATTCTTTTTGGTTAGTCAGCTGGT 1140 4133 CCCGCAACCTGCAAATCTTAAAATAGACTCAAATTCTTTTTTTT	1321   IGATAAAGCATATAATCTGTAACTGAGGCTCATAAAGCCTTGTTTGAAATAAGGGTCG   1380     4373   IGATAAAGCATATAACTGAGGGCTCATAAAGCCTTGTTTGAAATAAGGGTCG   4432     4433   TAATTCTGATTTCCAAGCCTTAAACTGAGGCCTTGATGAAATAAGGGTCG   4492     4433   TAATTCTGATTTCCAAGCCTTAAAATTATTAGAACGCTTGAATGAA

Qy         2221 AGTAACGGATTCTAGTCTGAAAGCCAATGCAACAGAACTCTAGCTGGTTTACGAAATAA         2280           Db         2238 AGTAACGGATTCTAGTCTCAAAGCCAATGCAACACAAACTCTAGCTGGTTTACGAAATAA         2297           Qy         2281 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAAAATTACTTGC         2340           Db         2298 TTTGACTCTTCAAATTATGGATAACAATAGTATCATGGCAGAAGAAATTACTTGC         2357           Qy         2341 GTTGTTAAAAGGAAGTAACCATTGTTAAGGAAAAATAAAC         2389           HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	RESULT 8 AR218862 LOCUS Sequence 94 from patent US 6420135. ACCESSION AR218862 VERSION AR218862 VERSION AR218862 VERSION AR218862.1 GI:23319796 KEYWORDS SOURCE Unknown. Unclassified. URases 1 to 8195) AUTHORS Kunsch, C.A., Choi, G.H., Dillon, P.S., Rosen, C.A., Barash, S.C., Fannon, M.R. and Doughberty, B.A. TITLE Streptococcus pneumoniae polymuclectides and sequences JOURNAL Patent: US 6420135-A 94 16-JUL-2002;	FEATURES	Db   3053   TTCTTACGAGTTGGGACTGTATCAAGCTTAAGGAAATAATGGTTTCCTA   3112	24 TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATAATGATGATGATGATGATGATGATGA
1098   CCCGCAACCTGCACCAAATCTTAAAATAGACTCCAAATTCTTCTTTTGGTTAGTCAGCTGGT   1157     1141   ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAAAGGGCATCTCTCGTTAGTCTTTGC   1200     1158   ACGAAAAGTTGGGGAAGGATATGTATTCGAAGAAGAAGAAGACTCTCTCGTTATGTCTTTGC   1217     1201   GAAAAGTTGGGAAGAAGTGTTAAAAATCTTGAAAAGAAGAAACTATCAAAAAAAA	1321 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGNAATAAGGGTCG 1380  1338 TGATAAAGCATATAATCTGTTAACTGAGGCTCATAAAGCCTTGTTTGAAATAAGGGTCG 1397  1381 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGATGAATCGACTAA 1440  1398 TAATTCTGATTTCCAAGCCTTAGACAAATTATTAGAACGCTTGAATGATGAATCGACTAA 1457  1441 TAAAGAAAAATTCCAAGCCATTAGACAATTATTAGAACGCTTGAATGAA	1561 AGCTGATAAGTATACAACGTCAGATGGTTACATTTTTGATGAACATGATATAATCAGTGA 1620	1741 TCCATCTCCAGACGCAGATGTTAAAGCAAATCCAACTGGAGATAGTGCAGCAGCTATTTA 1800	1921   TARATITGCTTGGTTTGATGATCACATACAAAGCTCCAAATGGCTATACCTTGGAAGA   1980   1938   TARATITGCTTGGTTTGATGATCACATACAAGCTCCAAATGGCTATACCTTGGAAGA   1991   1938   TARATITGCTTGGTTAGTACACATACACATCCTAAAAGA   1997   1981   TITGTTTGCTTGGTTAACACACATACACACAAAACACACATCTAATGA   2040   1998   TITGTTTGCGACGATTAAGTACTACGAACACACCTGACGAACGTCCACATTCTAATGA   2041   TGGATGGGGCAATGCCAGTGAGAACACCCTGACGAACGTCCACATTCTAATGA   2057   2041   TGGATGGGCCAATGCCAGTGAGAACACCCCACATCTAATGA   2057   2058   TGGATGGGCCAATGCCAGTGAGCAAGACACACACATCAAAAAAAA

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1097 CCCGCBACCTGCACCAATCTTAAAATAGACTCAAATTCTTCTTTGGTTAGTCAGCTGGT 1140 GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG 1020 240 480 540 009 099 720 737 780 797 840 857 900 917 960 120 180 300 317 360 420 497 557 617 677 137 197 257 377 437 17 AGCAAGTCAAAGTAATGACATTGATAGTCTCTTGAAACAGCTCTACAAACTGCCTTTGAG GTCTGAATTGGAAGAACGAATCGCTCGTATTATTCCCCTTCGTTATCGTTCAAACCATTG GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACGGAACCTAGTCCAGG 138 GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC 198 ITCACATGGCGACCACTATCATTATACAATGGTAAGGTTCCTTATGACGCTATCATCAG 258 IGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTATTGT TTCAAGAACCTATCGCCGACAAAATAGCGATAACACTTCAAGAACAAACTGGGTACCTTC TGTAAGCAATCCAGGAACTACAAATACTAACAAGCAACAACAGCAACACCAACAGTCA 918 AGCTAGAGGTGTTGCAGTGCCACAGAGATCATTACCACTTCATCCCTTACTCTCAAAT GGTACCAGATTCAAGGCCAGAACAACCAAGTCCACAACCGACTCCGGAACCTAGTCCAGG TATAGATGGAAAACAAGCGACGCAAAAAACGGAGAATTTGACTCCTGATGAGGTTAGCAA 318 GGTCAAGGGTGGATATGTTATCAAGGTAGTAGAAAAAAATACTATGTTTACCTTAAGGATGC TCAACATCGTGAAGGTGGAACTCCAAGAAACGATGGTGCTGTTGCCTTGGCACGTTCGCA 498 AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 601 ATCAGCTAGCGAGTIGGCTGCTGCAGAAGCCTTCCTATCTGGTCGAGGAAATCTGTCAAA TCAACGACATGTAGAATCTGATGGCCTTGTCTTTGATCCAGCACAAATCACAAGTCGAAC AGCTAGAGGTGTTGCAGTGCCACACAGGAGATCATTACCACTTCATCCCTTACTCTCTCAAAT GCGTGAAGGAATCAATGCTGAGCAAATCGTCATCAAGATAACAGACCAAGGCTATGTCAC TICACATGGCGACCACTATCATTACAATGGTAAGGTTCCTTATGACGCTACATCAG TGAAGAATTACTCATGAAAGATCCAAACTATAAGCTAAAAGATGAGGATATTGTTAATGA GGTCAAGGGTGGATATGTTATCAAGGTAGATGGAAAATACTATGTTTACCTTAAGGATGC AGGACGCTATACTACAGATGATGGTTATATCTTTAATGCTTCTGATATCATAGAGGATAC 558 TGGTGATGCTTATATCGTTCCTCATGGAGATCATTACCATTACATTCCTAAGAATGAGTT 738 361 421 618 678 1021 1038 1081 181 481 721 781 198 841 828 901 961 978 241 541 661 18 61 121 301 8 8 8

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 90 summaries

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1: gb\_ba:\*

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7: gb\_mi:\*

8: gb\_m 66.1 100.1 1 Database :

Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR120265 Sequence	53274	048 Streptoc	11695	19139 Seque	3774	7418 Streptoc	11763 Sequenc	19937 Streptoc	19951 Streptoc	0221 3585	3072 5	290 N	9970 Human c	9971	270 Sequence	1961 Sequence	3279 Strepto 3011 Semienc	, щ	154 Streptoc	72	191 Strepto	785	46 Streptoc	49 Strept 45 Semien	48 8	91 1	3.4	4.0		52 Sequence	23	5 Polynucl	31	45 Strepto	97 Sequenc	4 4 7	43 Streptoc	42 Sequenc	11096	53414 Strepto	268044 Strepto	344443	343114 Sequenc	263615 Novel s	AK34116 Sequence AR120328 Sequence
SUMMARIES ID	AR120265 AR340956	332	80	116	100	37	74	AX5/1763 AE008479	SPNEU1915	8 5	AF340221 BD263585	-:	AX343073		AF3400	70	w .			41 (*	,	O1 U	11 (	4	ਹ ਹਾ	<b>4</b> (	σΓ	. 0	AE008464 CDNE111 007	SPNEU1901	AX571762	١	BD004035						AR344442 AR120405			40807	1989	311	336	203
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QY         562 SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT 621           DD         302 SEABRAAQAYAKKGITPFSTDHQDSGNTEAACGAEAIYNRVKAAKVPLDRMPYNLQYT 361           QY         622 VEVKNGNLIIPHYDHYHNIKPEMPDDHTYKAAPNGYTLEDLEATIKYYVEHDDERPHSNDG 681           DD         362 VEVKNGNLIIPHYDHYHNIKPEMPDEGLYEAPKGYTLEDLEATIKYYVEHPDERPHSNDG 421           QY	RESULT 25  US-10-324-143-26  Sequence 26, Application US/10324143  Febblication No. US20030232976A1  GENERAL INFORMATION: APPLICANT: HAMEL, JOSEE APPLICANT: HAMEL, JOSEE APPLICANT: MARTIND, NATHALIE APPLICANT: MARTIND, STRENARD R. APPLICANT: MARTIND: STRENARD R. APPLICANT: OUGLETTE, CATHERINE TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS FILE REFERENCE: 55190-56 CURRENT FILING DATE: 2002-12-20 PRIOR PELING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 160 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 26 LENGTH: 555 LENGTH: 555 TYPE: PRI CATHERINE FRATURE: OTHER INFORMATION: Description of Artificial Sequence FRATURE: OTHER INFORMATION: modified Streptococcus pneumoniae protein sequence US-10-324-143-26	Query Match         45.3%; Score 1888; DB 15; Length 555;           Best Local Similarity 65.7%; Pred. No. 1.8e-127;         Anteles 34; Gaps 3;           Matches 364; Conservative 59; Mismatches 97; Indels 34; Gaps 3;         326           DD LOBLIKQLYKLPLSQRHVESDGLVPDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE 60         326           DD DIDSLIKQLYKLPLSQRHVESDGLIFDPAQITSRTARGVAVPHGDHYHFIPYEQMSELEK 60         326           QY         326           RIARIIPLRYKSNHWVPDSRPEGPSPORPORPERSPROMPHDEKLUKSAVR 120           QY         332           KRANIIPLRYKSNHWVPDSRPEEPSPORPAPROPAPROPAPROPERSUNT 120           QY         332           KVGGGYVFEERGISRYVFAKDLPSETVKNLESKLSKOESVSHTLTAKKENVARRAVR 120           QY         442           KAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTHKELVDDLIAFLAPITHPERL 501           Db         121           KVGGGYVFEENGVSRYIPAGALDKLLERLKDVSSDKVKLVDDLIAFLAPITHPERL 240           QY         442           KAYDLLARIHODLLDNKGRQVDFEALDNLLERLKDVSSDKVKLVDDLIAFLAPITHPERL 240           QY         502           GKPNSQLEYTEDEVRIAQCRATTSDGYIFDBEDIISDEGDAYVTPHMGHSHWIGKDSL 561           LIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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682 WGNASEHVLGKKDHSEDPNKNFKAD-----EBPVE 711
                                                                        772 MAEAEKLIALLKGS 785
                                                                               541 MAEAEKLLALLKES 554
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Cy SEZ SDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYNVEHT 621	December   Colored   Col
	Sequence 315. Application NS/9884465A  Sequence 315. Application NS/9884465A  GENERAL INFORMATION: BEALLOANT: Shire Biological Shire Blooder. Inc. APPLICANT: Brine Blooder. Bernard APPLICANT: Broder. Laterand APPLICANT: Broder. Streptcoccota Attigens TILE DETERMENT: ON Streptcoccota Attigens TILE REPERMENT: ON Streptcoccota Attigens TILE APPLICANT: MUMBER: 05/10,6520  FRICK FILING DATE: 2001-06-20  F

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266 DIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEE 325
                                                                                                              62 RIAKIIPLRYRSNHWVPDSRPEEPSPQPTPEPSPSPQPAPNPQPAPSNPIDEKLVKBAVR 121
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                                       422 FGNASDHVQRNKNGQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPPE 481
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                                                                                                                                                                                                                                                                                                                            GRUERENT FIRST AND STATES AND SEQUENCE STATES APPLICANT: HAMEL, JOSEE APPLICANT: CHARLAND, NATHALIE APPLICANT: CHARLAND, NATHALIE APPLICANT: MARTHY, DENIS APPLICANT: MARTHY, DENIS APPLICANT: MARTHY, DENIS APPLICANT: MOTERATE, CATHERINE APPLICANT: OUTLETPE, CATHERINE STILE REFERENCE: 55190-56 CURRENT APPLICATION NUMBER: US/10/324,143 CURRENT FILING DATE: 2002-12-20 PRIOR PILING DATE: 2002-12-20 PRIOR FILING DATE: 2001-12-20 PRIOR FILING DATE: 2001-12-20
                                                                                                                                                                           772 MAEAEKLLALLKGSNPSSVSKEKI 795
WGNASEHVLGKKDHSEDPNKNFKAD-
                                                                                                                                                                                                                     542 MAEAEKLLALLKESKXXDLTEEQI
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 54
LENGTH: 1126
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64.9%; Pred. No. 8.5e-128;
iive 63; Mismatches 101;
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NAME/KEY: MISC, FEATURE
LOCATION: (1) _ (1)
OTHER INFORMATION: Xaa = Methionine or nothing
                                                                                                                                            SQUENCE 1903-79 Application US/09884465A
Publication No. US20030077293A1
GENERAL INFORMATION:
APPLICANT: Shire Biochem, Inc.
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Martin, Denis
APPLICANT: Ouellet, Catherine
TILLE OF INVENTION: Streptococcus Antigens
FILE REPERRNCE: 055190-0044
CURRENT FILING DATE: 2001-06-20
FRIOR FILING DATE: 2001-06-20
FRIOR FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (557)..(557)
OTHER INFORMATION: Xaa = Glycine or nothing
NAME/KEY: MISEERIURE
LOCATION: (558)..(558)
OTHER INFORMATION: Xaa = Proline or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 64.9%
Matches 366; Conservative
785
                                       501 EAEKLLALLKES 612
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EAEKLLALLKGS
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SEQ ID NO 383
LENGTH: 1126
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541 PEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNAKKTLTGLKNNLLFGTQDNNTIMA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: modified Streptococcus pneumoniae protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%; Score 2170; DB 15;
68.5%; Pred. No. 9.2e-148;
7ative 59; Mismatches 100;
                                                                        Sequence 2.2, Application US/10324143
Publication No. US20030232976A1
GENERAL INFORMATION:
APPLICANT: HAMEL, JOSEB
APPLICANT: CHARLAND, NATHALIE
APPLICANT: BRODERN, BERNARD R.
APPLICANT: BRODERN, STREPTOCOCCUS ANTIGENS;
APPLICANT: BLAIS, NORMAND
APPLICANT: BLAIS, NORMAND
APPLICANT: BLAIS, NORMAND
APPLICANT: CURLETTE, CATHERINE
ITILE REFERENCE: 51190-56
CURRENT APPLICATION NUMBER: 60/341,252
PRIOR FILING DATE: 2002-12-20
PRIOR PRILIG DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2:
LENGTH: 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NASEHVLGKKDHSEDPNKNFKAD-
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 2649.5; DB 9; Length 763; 66.8%; Pred. No. 3.1e-182; artive 77; Mismatches 132; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG-
                                  NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: BB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-765-272-66
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH, 763 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                             TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
FILING DATE: <Unknown>
                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.8%
Matches 519; Conservative
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141 AAHADNIRTKEEIKRQKQEHSHNHNS----RADNAVAARRAQGRYTTDDGYIFNASDIIED 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- DPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEV
                                                                                                                    LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFD
                                                                                                                                                                                                                                                                                                                                                                                  180 TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVP
                                                                 ----KQGSRPSSSSYNA
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                                                                                                                                                                                                                                  ----PGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLES
                                                                                                                                                                                                                                                                                                  KLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLER
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                                                                                                 240 SVSNPGTINTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVBSDGLVFDPAQITSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDGS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences, Inc
                                                        APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <UNKNOWN>
CAPPLICATION DATA:
APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Human Genome Scie:
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
US-09-765-272-66
; Sequence 66, Application US/09765272
; Patent No. US/002061545A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville STATE: Maryland
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                                                          SLQPAPNPQPAPSNPID--EKLVKEAVRKVGDGYVFEENGVSRYIPAKDLSAETAAGIDS
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APPLICANT: HAMEL, JOSEE
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: BLAIS, NORMAND
APPLICANT: BLAIS, NORMAND
APPLICANT: STAFF CATHERINE
TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 55190-56
CURRENT APPLICATION NUMBER: US/10/324,143
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PRIOR APPLICATION NUMBER: 60/341,252
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9
LENGTH: 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/10324143 Publication No. US20030232976A1 GENERAL INFORMATION:
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64.5%; Pred. No. 1.8e-189;
iive 90; Mismatches 145; Indels
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APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: Brodeur, Bernard
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Charland, Nathalie
APPLICANT: Outellet, Catherine
TILLE OF INVENTION: Streptococcus Antigens
FILE REFERENCE: 055190-004
CURRENT APPLICATION NUMBER: 05/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLICATION NUMBER: 60/212,683
PRIOR APPLIANG DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 384
SOFTWARE: PatentIn version 3:1
                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/09884465A; Publication No. US20030077293A1; GENERAL INFORMATION:
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APPLICANT: HAMEL, JOSEE
APPLICANT: GHARLAND, NATHALIE
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: BALAIS, NORMAND
APPLICANT: BLAIS, NORMAND
APPLICANT: OUBLETTE, CATHERINE
TITLE OF INVENTION: STREPPOCOCCUS ANTIGENS
FILE REFERENCE: 55190-56
CURRENT APPLICATION NUMBER: US/10/324,143
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/341,252
PRIOR APPLICATION NUMBER: 60/341,252
PRIOR APPLICATION NUMBER: 60/341,252
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VEY: 2.1
                     Sequence 32, Application US/10324143
Publication No. US20030232976A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                SYELGLYQARTV-KENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
                    Gaps
                    26;
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 Length
                    Indels
 Score 2772; DB 15;
Pred. No. 5.2e-191;
                    91; Mismatches 144;
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66.6%;
                    Conservative
 Query Match
Best Local Similarity
Matches 541; Conserv
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US-10-387-783-4
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APPLICANT: Johnson, Leslie S.
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneuumoniae Polypeptides Having Selected Structural
TITLE OF INVENTION: Motifs

FILE REFERENCE: 469201-683

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                                                                                                                                                       Query Match 66.6%; Score 2772; DB 15; Best Local Similarity 65.0%; Pred. No. 5.2e-191; Matches 541; Conservative 91; Mismatches 144;
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CURRENT FILING DATE: 2003-03-13;
PRIOR APPLICATION UNBER: 094468,656;
PRIOR FILING DATE: 1999-12-21;
PRIOR PILING DATE: 1998-12-21;
NUMBER OF SEQ ID NOS: 14;
SEQ ID NO 4;
SEQ ID NO 4
                                                                                                                     ; ORGANISM: Streptococcus pneumoniae US-10-387-783-4
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RESULT 12
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LENGTH: 819
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J. RAPELICANT: Johnson, Leslie S.

APPLICANT: Johnson, John E.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

TITLE OF INVENTION: Motifs

FILE REFERENCE: 469201-686

CURRENT FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: 09/468,656

PRIOR APPLICATION NUMBER: 60/113,048

PRIOR PLING DATE: 1999-12-21

PRIOR PLING DATE: 1998-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver: 3.0
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                                                              TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                   Sequence 10, Application US/10412850 Publication No. US20040001836A1 GENERAL INFORMATION:
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US-10-412-850-10
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184 DKVKLVEDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTAEDGYIFDPRDITS
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                                                                              YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLE
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APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pocine Compositions Comprising Streptococcus
TITLE OF INVENTION: Motifs
FILE REFERENCE: 469201-683
CURRENT APPLICATION NUMBER: US/10/387,783
CURRENT APPLICATION NUMBER: 09/468,656
PRIOR APPLICATION NUMBER: 09/468,656
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
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66.7%; Pred. No. 3.2e-192;
iive 85; Mismatches 139; Indels
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SOFTWARE: PatentIn Ver. 3.0
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Best Local Similarity 66.7
Matches 544; Conservative
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; OKGANISM: SL.
US-10-412-862-10
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                                                                                                   Query Match 67.1%; Score 2795; DB 10; Best Local Similarity 67.0%; Pred. No. 1.1e-192; Matches 549; Conservative 83; Mismatches 139;
                                                                    ORGANISM: Streptococcus pneumoniae
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: Patentin Ver. 2.1
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US-09-769-787-194
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US-10-412-862-10
                                SEQ ID NO 194
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TYPE: PRT
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66.7%; Pred. No. 3.2e-192;
ive 85; Mismatches 139; Indels
                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Streptococcus pneumoniae
US20040052781A1
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Matches 544; Conservative
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Gaps 4, 09 61 180

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Description of Artificial Sequence: Synthetic modified Streptococcus pneumoniae protein sequence
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                                                              ; Score 2961; DB 15;
; Pred. No. 8.7e-205;
54; Mismatches 75;
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Publication No. US20030091577A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE REFERENCE: PWC/P21129W0
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR PLILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
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80.7%;
                                                                 Query Match
Best Local Similarity 80.7
Matches 556; Conservative
OTHER INFORMATION: OTHER INFORMATION:
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                    ; OTHER INFORM
US-10-324-143-38
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                               141 AHADNVRTKEEINRQKQEHSQHREGGTSANDGAVAFARSQGRYTTDDGYIFNASDIIEDT
                                                                               VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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APPLICANT: CHARLAND, NATHALIE
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: BLAIS, NORMAND
APPLICANT: BLAIS, NORMAND
APPLICANT: OUELETTE, CATHERINE
TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS
FILE REPERENCE: 55190-56
CURRENT APPLICATION NUMBER: US/10/324,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 2002-12-20
PRIOR APPLICATION NUMBER: 60/341,252
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 38
LENGTH: 690
TWONETH: 60
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ORGANISM: Artificial Sequence
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US-10-324-143-38
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099   091   092   092   093   094   095	; TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS ; FILE REFERENCE: 55190-56 ; CURRENT APPLICATION NUMBER: US/10/324,143 ; CURRENT FILING DATE: 2002-12-20 ; PRIOR FILING DATE: 2001-12-20 ; NUMBER OF SEQ ID NOS: 160 ; SOFTWARE: PATENTIN VEr. 2.1 ; SEQ ID NO 8 ; LENGTH: 840 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FRATURE: ; OTHER INFORMATION: Description of Artificial Sequence ; OTHER INFORMATION: modified Streptococcus pneumoniae protein sequence US-10-324-143-8	Query Match         77.3%;         Score 3218;         DB 15;         Length 840;           Best Local Similarity 75.2%;         Pred. No. 3.3e-223;         Indels 34;         Gaps 3;           QY         1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT 60           21 AYELGLHQAQTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT 80           QY         61 SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120           QY         61 SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA 120           DD         81 SHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNGKYYVYLKDA 140
	Olm 5	OY 181 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVPS 240  Db 201 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRENLSNLRTYRRONSDNTFRTNWVPS 260  OY 241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300  Db 261 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLIFDPAQITSRT 320  OY 301 ARGVAVPHGDHYHFIPYSQASGSNDIDSLLKQLYKRPLSGRHVESDGLIFDPAQITSRT 320  ON 301 ARGVAVPHGDHYHFIPYSQASELEERIARIIPLRYRSNHWVPDSRPEPPSPG 360  Db 321 ARGVAVPHGNHYHFIPYSQASELEERIARIIPLRYRSNHWVPDSRPEFPSPG 380

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PQPAPNPQPAPSNPIDEKLVKEAVRKVGDGYVFEENGVSRYIPAKNLSAETAAGIDSKLA 421
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                                                                                                                                                                                                                                APPLICANT: HAMEL, JOSEE
APPLICANT: CHARLAND, NATHALIE
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: BRODEUR, BERNARD R.
APPLICANT: MARTIN, DENIS
APPLICANT: MOLEGATE, CATHERINE
APPLICANT: GUELGATE, CATHERINE
TITLE OF INVENTION: STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 55190-56
CURRENT APPLICATION NUMBER: US/10/324,143
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/341,252
PRIOR FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PATENTIN VENTION OF 160
                                                                                                                                                                       Sequence 19, Application US/10324143
Publication No. US20030232976A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
                781 LLKGSNPSSVSKEKIN
                                                   801 LLKGSNPSSVSKEKIN
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Matches 616; Conservative
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US-10-324-143-19
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99.9%; Pred. No. 1.9e
iive 0; Mismatches
TITLE OF INVENTION: Preumoniae Polypeptides
TITLE OF INVENTION: Motifs
FILE REPERENCE: 46501-633
CURRENT APPLICATION NUMBER: US/10/387,783
CURRENT FILING DATE: 2003-03-13
RIOR APPLICATION NUMBER: 094468,656
PRIOR FILING DATE: 1999-12-21
PRIOR RILING DATE: 1999-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-21
SOFTWARE: PATCH IN VOMBER: 60/113,048
                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Streptococcus pneumoniae US-10-387-783-8
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Best Local Similarity 99.9
Matches 795; Conservative
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                                                                                    100.0%; Score 4163; DB 15
99.9%; Pred. No. 1.9e-291;
tive 0; Mismatches 1;
                         ; ORGANISM: Streptococcus pneumoniae US-10-412-850-8
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Selected Structural
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APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Stritific OF INVENTION: Pneumoniae Polypeptides Having Sell: TITLE OF INVENTION: Motife FILE OF INVENTION: MOTIFE OF INVENTION: MOTIFE OF INVENTION DATE: 2003-04-14 PRIOR APPLICATION NUMBER: 09/468,656 PRIOR APPLICATION NUMBER: 06/113,048 PRIOR FILING DATE: 1999-12-21 PRIOR FILING DATE: 1999-12-21 NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 3.0
SEQ ID NOS SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/10412850; Publication No. US20040001836A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLKGSNPSSVSKEKIN 796
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US-10-412-850-8
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Sequence 8, Application US/10412862
; Sequence 8, Application US/10412862
; Publication No. US20040052781A1
; GENERAL INFORMATION:
; APPLICANT: Adamou, John E.
; APPLICANT: Adamou, John E.
; TITLE OF INVENTION: Pneumoniae Polypeptides Having Streptococcus
; TITLE OF INVENTION: Motifs
; TITLE OF INVENTION: Motifs
; TITLE OF INVENTION: Motifs
; FILE REPERBNCE: 468201-685
; CURRENT APPLICATION NUMBER: US/10/412,862
; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/413,048
; PRIOR APPLICATION NUMBER: 60/113,048
; PRIOR APPLICATION NUMBER: 60/113,048
; RIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360
                                                                                                                                                                                            VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
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24. VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 300
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                                                                                                                                                                 POPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
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99.9%; Pred. No. 1.9e-291;
ive 0; Mismatches 1;
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Best Local Similarity 99.9
Matches 795; Conservative
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US-10-412-862-8
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Sequence 2, Appli
Sequence 114, App
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <a href="https://documents.com/">CLASSIFICATION: <a href="https://documents.com/">Documents.com/</a>
US-10-324-143-2
US-10-324-143-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                            ALIGNMENTS
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                 Sequence 56, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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  15
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Matches 796; Conservative
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272
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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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Sequence 32, Appli
Sequence 6, Appli
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Sequence 22, Appl
Sequence 33, Appl
Sequence 34, Appl
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Sequence 31, Appl
Sequence 31, Appl
Sequence 51, Appl
Sequence 52, Appl
Sequence 37, Appl
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Sequence 37, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 36, Appl
Sequence 6, Appl
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                                                                   US-09-765-272-66

US-09-765-272-66

US-10-324-143-22

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US-09-789-736-18

US-09-769-13

US-10-324-143-39

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Sequence 38,
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                              GenCore version 5.1.6
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Listing first 90 summaries
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App Appl Appl Appl Appl

Db   1661 ASTTDHSDRSLRGFDLDWTTDSSSTASDTMSLPSLQSCDIDSIXEPMAPIVV 1712   Qy   280 - SQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYKSN 338	394 1812 451 1921 1921 591 2028 609 arch comple <sup>†</sup> b time : 36	
	US-09-466-777-2  US-09-466-777-2  US-09-466-777-2  US-09-466-777-2  US-09-466-777-2  Sequence 2, Application US/08466277  Patent No. 6190666  APPLICANT: Garoff, Henrik  Liljestrom, Peter  TITLE OF INVENTION: DNA Expression Systems Based on  NUMBER OF SEQUENCES: 27  CORRESPONDENCE ADDRESS: 27  CORPUTER: Palls Church  STARE: P.O. Box 747  CITY: Palls Church  COMPUTER: TEADAGLE FORM:  MODUTINER: IBM PC compatible  COMPUTER: SEDDAGLE FORM:  MODUTINER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: NEADAGLE FORM:  MEDICATION NUMBER: US/08/466,277  PILICATION NUMBER: 07/20,281  PILICATION NUMBER: 07/20,281  PILICATION NUMBER: 08/20,281  PILICATION NUMBER: 08/20,281  TELEPROMAUTION TOWNEATION:  TELEPROMAUTION: COMPATION:  TOWNEATION TOWNEATION:  TELEPROMAUTION: COMPATION:  TOWNEATION: COMPATION: COMPATION:  TOWNEATION: COMPATION: COMPATION:  TOWNEATION: COMPATION: COMPA	Query Match

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                                                                                                   COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/920,281C

FILING DATE: 13-AUG-1992

CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                                                                 COUNTRY:
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1366 SVPIGNGHVAITAVSPHRDGSVTSTKLLFPSKATSELSHSAKSDAGLVGGGEDGDTDDDG
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                                                                                                              GKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVAL-
1717 TEE--FETLKEFYQEVQSCTVDLGITADSSNHPDNK-HKN 1753
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| Patent No. 5739026
| GENERAL INFORMATION: BAPLICANT: Liljestrom, Peter APPLICANT: Liljestrom, Peter ITLE OF INVENTION: DNA Expression Systems Based on ITLE OF INVENTION: DNA Expression Systems Based on ITLE OF INVENTION: Alphaviruses NUMBER OF SEQUENCES: 27
| CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
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OTHER INFORMATION: Glycosylation; N-linked (GLCNAC ...) (potential)
NAME/KEY: TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (potential)
LOCATION: (602)..(602) OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
                                                                                                                                                     (potential)
                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
COCATION: (677).
OTHER HIPPRMATION: Glycosylation; N-linked (GLCNAC...) (potential)
NAME/KEY: VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1456)..(1456)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
COCKTION: (1017). (1017)
COTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1082)..(1082)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
NAME/KEY: SITE
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Best Local Similarity 19.2%; Pred. No. 0.14;
Matches 169; Conservative 113; Mismatches 267; Indels 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (755)..(1614)
OTHER INFORMATION: Splicing variant; missing (in short isoform)
NAME/KEY: BINDING
                                                                  NAME/KEY: SITE
LOCATION: (629)...(629)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1122)..(1122)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...)
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1561)..(1561)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC
                                                                                                                                                                                NAME/KEY: BINDING
LOCATION: (637)...(637)
OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1550)..(1550)
OTHER INFORMATION: Chondroitin sulfate (potential)
NAME/KEY: SITE
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OTHER INFORMATION: Transmembrane region; potential NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (997)..(997)
OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1548)..(1548)
OTHER INFORMATION: Chondroitin sulfate (potential)
NAME/KEY: BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1744)..(1997)
OTHER INFORMATION: Protein-tyrosine phosphatase
NAME/KEY: ACT SITE
LOCATION: (1932)..(1932)
OTHER INFORMATION: Active site; by similarity
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1998)..(2314)
OTHER INPORMATION: Protein-tyrosine phosphatase
NAMF/KEY: misc feature
LOCATION: (2222)..(2222)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1662)...(2314)
OTHER INFORMATION: Cytoplasmic (potential)
NAME/KEY: CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DUCATION: (2222)
; OTHER INFORMATION: Ancestral active site
US-09-816-703A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1722)..(1728)
OTHER INFORMATION: Missing (in ref. 2)
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1050).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: Reference
LOCATION: (1)..(2314)
OTHER INFORMATION: The phosphatase, FTP zeta, is expressed in brain and has an N-term OTHER INFORMATION: inal receptor domain homologous to carbonic anhydrases; Proc. Nat OTHER INFORMATION: 1. Acad. Sci. USA 89 (16), 7417-7421 (1992
NAME/KEY: Reference
NAME/KEY: Reference
NAME/KEY: Reference
                       APPLICANT: Melcher, Thorsten
APPLICANT: Melcher, Sabine
APPLICANT: Meller, Sabine
APPLICANT: Chin, Daniel
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a Biomolecular Target
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a Biomolecular Target
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as a Biomolecular Target
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TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Seta as a Biomolecular Target
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Seta as a Biomolecular Target
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Seta Associated Phosphatase Seta Associated Phosphatase Seta Associated Phosph
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OTHER INFORMATION: Levy, J.B., et al.; The cloning of a receptor-type protein tyrosi OTHER INFORMATION: ne phosphatase expressed in the central nervous system; J. Biol. OTHER INFORMATION: Chem. 268 (14), 10573-10581 (1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (25)..(1635)
OTHER INFORMATION: Extracellular (potential)
NAME/KEY: misc_feature
LOCATION: (25)..(2314)
OTHER INFORMATION: Mature chain; protein-tyrosine phosphatase zeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE

LOCATION: (223)..(223)

OTHER INFORMATION: Glycosylation, N-linked (GLCNAC...) (potential)

NAME/KEY: SITE

LOCATION: (232)..(232)

OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (134)..(134)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
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LOCATION: (552)..(552)
OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
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DTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
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OTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
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NTHER INFORMATION: Glycosylation; N-linked (GLCNAC...) (potential)
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OTHER INFORMATION: Chondroitin sulfate (potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATION: (34)..(302)
THER INFORMATION: Carbonic-anhydrase like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OCATION: (312) ..(406)
THER INFORMATION: Fibronectin Type-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(24)
OTHER INFORMATION: By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
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12 VKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHY 66	160 LQENKSVVNVQPTNEENKKVDAKTESTTLNVKSDAIKSNDETLYDNNSNSN 210	67 HYYN	211 NENNADIILPKSTAPKRLNTRMRIAAVQPSSTEAKNVNDLITSNTTLTVVDADKNNKIVP 270	92LKDEDIVNE-VKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQH 142	271 AQDYLSLKSQITVDDKVKSGDYFTIKYSDTVQVYGLNPEDIKNIGDIK 318	143 REGGIPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHY 194	319DPNNGETIATAKHDTANNLITYTFTDYVDRFNSVQMGINYSIYMD 363	195IPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVDSVS- 242	:   ::   : :   364 ADTIPVSKNDVEFNVTIGNTTTKTTANIQYPDYVVNEKNSIGSAFTETVSH 414	243NPGTININISNINSNINSQASQSNDIDSLLKQLYKLPLSQ 281	415 VGNKENPGYYKQTIYVNPSENSLINAKLKVQAYHSSYPNNIGQINKDVTDIKIYQVPK 472	282 RHVESDGLVFDPAQITSRTARGV-AVPHGDHYHFIPYSOMSELEERIARIIPLRYRSNHW 340	473 GYTLNKGYDVNTKELFDVTNQYLQKITYGDNNSAVIDFGNADSAYVVWVNTKEQYTN- 529	341 VPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRRKVGEGYVFE- 390	530SESPTLVQMATLSSTGNKSVSTGNALGFTNNQSGGAGQEVYKIG-NYVWED 579	391SKGISRYVSETVK 409	580 TNKNGVQELGEKGVGNVTVTVFDNNTNTKVGEAVTKEDGSYLIPNLPNGDYRVEFSNLPK 639	410 NLBSKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRN 461	640 GYEVTPSKQGNNEELDSNGLSSVITVNGKDNLSADLGIYKPKYNLGDYVWEDTNKNGIQD 699	462 SDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDE 514	700 QDEKGISGVIVTLKDENGNVLKIVITDADGKYKFTDLDNGNYKVEFTIPEGYI 752	515 -VRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAA 569	753 PITVISGSDIEKDSNGLTITGVINGADNMILDSGFYKTFKYNLGNYVWEDTNKDGKQDST 812	570 QAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNL 629	813EKGISGSGVIVILKNENGEV 830	630 IIPHK-DHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGN 684	831 LQTTKTDKDGKYQFTGLENGTYKVEFETPSGYTPTQVGSGTDEGIDSNGT 880	685 ASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEK 726	881 STTGVIKDKDNDTIDSGFYKPTYNLGDYVWEDTNKNGVQDKD922	727 VEAQLKEAEVLLAKVTDSSLKANATETLAGLRINILTLQIMDINSIMAEAEKLLALLKGSN 786	923 -EKGISGVTVTLKDENDKVLKTVTTDENGKYQFTDLNNGTYKVEFETPSGYT 973	787 PSSVS 791	974 PISVI 978	RESULT 23 US-09-816-703A-2 ; Sequence 2, Application US/09816703A
ζ	q <sub>Q</sub>	ò	qq	δ	qq	λō	q	ò	Op	ζ	qq	δ	qq	ò	qq	δy	qa	δλ	qa	δλ	qq	δ	Ob	δ	qu	ò	qa	Qy	qa	ζ	qu	ογ	q	RES US-
:   AVREEPAYTEP 271	EQPSPQPTPEPS 358	QEPEHEGERXVEEEL 319	KVGEGYVFEE 391	EDYIVNGNVVET 379	YDKAYNLLTE 449	:: :   :   KKSITVSYNLIDTTS 431	-TH-PERLGKPN 505		HWIGKDŞLŞDKE 565	::    : RRYLSLSEAP 530	LPYMVEHT 621	:  :  ITENTDGTY 563	LFATIKY 667	LVTAMQSNLSGV 616	KADEEPVEET 713	AIYDLKKPLFDT 667	-KANATETLAGLRNNLTLOI 765	SVAGLVASAINTV 727								from Ctanhur occoning annuals	stapiiy totottus							1315; 331; Gaps 43;
: ;       : ;	Oy 299 RTARGVAVPHGDHYHFIPYSQMSELBERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS	Db 272 LATKGTQEPGHEGKATVREETLEYTEPVATKGTQEP	QY 359 PGPQPAPNLKIDSNSSLVSQLVR-	Db 320 PALEVITRNRTEIQNIPYTTEEIQDPTLLKNRRKIERGGQAGTRTIQYEDYIVNGNVVET	QY 392 KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLL-	Db 380 KEVSRTEVAPVNEVVKVGTLVKVKFTVEITNLTKVENKKS	KINDESTNKEKLVDDLLAFLAPI	Db 432 AYVSAKTQVFHG-DKLVKEVDIENPAKEQVISG-LDYYTPYTHLTYNLGENN	Qy 506 SQIEYTEDBVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKE	Db 485 EENTETSTQDFQLEYKKIEIKDIDSVELYGKENDRYR	QY 566 KVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMV	Db 531 TDTAKYFVKVKSDRFKEMYLPVKS	Qy 622 -VEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYT-LEDLFATI	Db 564 KVTVAVDQLVEEGTDGYKDDYTFTVAKSKAEQPGVYTSFKQLVTAMGSNLSGV	QY 668 YVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADE	Db 617 YTLASDMTADEVSLGDKQTSYLTGAFTGSLIGSDGTKSYAIYDL	QY 714 PAEPEVPQVETEKVEAGLKEAEVLLAKVTDSSLKANATET	DD 668 LNGATVRDLDIKTVSADSKENVAALAKAANSANINNVAVEGKISGAKSVAGLVASATNTV	Qy 766 MDWNSIMAEAEKLLALLKGSN 786	Db 728 IENSSFTGKLIANHQDSN 745	CC #11000	US-09-200-650E-5	; Sequence 5, Application US/USZUUBSUE ; Patent No. 6680195 ; Candon, Tubopakarion.	SENERAL INCONTINUE.		BICALINI, DELIGIE NI PERKINS, Samuel L. MIRMITAN: Extracellular Matrix-Dinding Droteins	VENITON: DATIACETHINA MACLIA-BINALIG FLOCETHS SINCE: D06283MS2/BAS SITCATTON MEMBED: 115/00/200 6505	CURKENI AFFLICATION NUMBER: US/09/200, 550E ; CURKENI FILING DATE: 1998-11-25	FILING DATE: 1997-11	; FRICK AFFLICATION NUMBER: 60/098,42/ PRICK FILING DATE: 1998-08-31	TWARE: Patentin Ver	SECTION 3	; TYPE: PKI: ; ORGALISKI: US-09-200-650E-5	Query Match 3.4%; Score 141.5; DB 4; Length Best Local Similarity 18.5%; Pred. No. 0.057; Matches 179; Conservative 128; Mismatches 327; Indels

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--LSEKSSIAADNLSSNDSFA 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 LKIEGYOYIGYIK-TKKODNTELSRTVDGKYSAORDSOPNSTKTSDVVHSADLEWNOGOG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DPAQITS 298
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 45.2
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 94 West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 AVALARSOGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFL
                                                                --KANATETLAGLRINLTLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.5%; Score 144; DB 4; Length 1040; Best Local Similarity 19.2%; Pred. No. 0.025; Matches 154; Conservative 111; Mismatches 284; Indels 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 IKVDGKYYV-YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRND-
                                                                  714 PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
NT APPLICATION DATA:
PEPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LVF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 118:
US-09-536-784-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                          766 MDNNSIMAEAEKLLALLKGSN 786
                                                                                                                                                                                      Sequence 118, Application US/09536784 Patent No. 6573082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: OCT-30-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1040 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 QLYKLPLSQRHVESDG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 KVSL---QGEASGDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                         RESULT 21
US-09-536-784-118
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                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                    PB340P2
                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PARTECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.5%;
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1040 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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Matches 154; Conserv
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QY 497 -HPERLGKPNSQIEYTEDEVRIAQL 520 ::	Qy 521 ADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGI 578  DD 754 VKTCTTSLNDADII-LSDYISDQKSKFESKQQDLIANIGKIVSNFLQEQNESLYTK 808	QY 579 LPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVK 625  DD 809ADILHSHLNDTNSNIRKANEIMNNRSEEFLRNAASQAEIVGANKERIQKTVE 860	Qy 626 NGNLIIPHKDH-YHNIKFAMFDDHTYKAPNGYTLEDLFATIKYYVEHPDERP 676  Db 861 NGSQLLDSKSKAIHSNSRSMYDHCLALAESQKQGVNLEVQTLDRLLQKVKE 911	Qy 677 HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEV 736  Db 912 HSEDNTKEKHQQLLDLLESLVGNNDNLIDSIKTPHTELQ 950	QY 737 LLAKUTDSSLKANATETLAGLRNNLTLQIMDNNSIMARAEKLLA 780	Oy 781 LLKGSNPSSVSKEKIN 796  Db 1008 TPSWIRDSSLIKETIN 1023	RESULT 19   Use - Compose

us-09-765-271-56.rai

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; Sequence 6, Application US/09723820; Patent No. 6468760; GENERAL INFORMATION:
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                                         781 LLKGSNPSSVSKEKIN 796
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182; Conserv
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CRGANISM: S.pombe
US-09-723-820-6
                                                                                                              RESULT 18
US-09-723-820-6
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Best Local S
Matches 182
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                                                                                                                                                                     GKQATQKTENLTPDEVSKREGINAE-----QIVIKI--TDQGYVTSHGDHYHYYN
                                                                                                             Query Match 3.5%; Score 145.5; DB 3; Length 1073; Best Local Similarity 18.6%; Pred. No. 0.02; Matches 182; Conservative 136; Mismatches 357; Indels 301;
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10
Windows Version 4.0
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OF SEQ ID NOS:
RE: FastSEQ for
                                                     TYPE: PRT
, ORGANISM: S.pombe
US-09-541-782-6
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APPLICANT: Sakowicz, Roman
APPLICANT: Sakowicz, Roman
APPLICANT: Baraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: 08/09/723,820
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 6
SEQ ID NO 6
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Patent No. 6617156
GENERAL INFORMATION:
PAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
FRIOR APPLICATION NUMBER: US 60/055,778
FRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 5178
                                                                                                                                                                NWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVES--DGLV--- 290
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                                                                                                                                                                                                            ----SVTEPAEHEEVVSEESNPEPAENEESSIEEAHQE--EIVPEQNDEESGESGLVDNE 131
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                                                                 EDIGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRIYRRQ--NSDNISRI
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Best Local Similarity 20.2%; Pred. No. 0.011;
Matches 141; Conservative 106; Mismatches 278; Indels
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ORGANISM: Enterococcus faecalis
US-09-134-000C-5178
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                                                                                                                                                                      166 D-DGYI----FNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAA-----EAFLS
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                                              224;
                                                                                     114 YVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVAL--ARSQGRYT
Query Match 3.5%; Score 146; DB 4; Length 1799; Best Local Similarity 19.9%; Pred. No. 0.042; Matches 156; Conservative 115; Mismatches 289; Indels 22
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APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
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; Sequence 6, Application US/09541782
; Patent No. 6284480
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Qy 99 NEVK-GGYVIKVDGKYYVYLK   :-	142 HREGGTPRNDGAVALARSQGRYT	Db 182 HYQQNTPIGDGPVLLPDNHYLSYQS Qy 190 DHYHYTPKNELSASEL	Db 234 MDELYKPRDEADSADLSLVDALTEPPPEIEGEI Oy 211 -FLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVS	294	QY 270 LLKQLYKLPLSQRHVESDGLVFDPAQITSR	DD 348 FLEERVDYÞDYGSSÓNWPEDASFCFQÞQÓVLDT OY 327 IARIIPLRYRSNHWVPDSRFBQPSPQPTPEPSP	Db 394 LADLLFVSSGPTNASAFTERDNFSEDSY	Oy 387 YVFEEKGISRYVFAKDLPSETVKNLESK	442 KAYNLLTEAHKALFXN	: :     1	Qy 498 PERLGKPNSQIEYTEDEVRIAQLADKYTTSDGY	Db 520EITKPDVILANVTQPSTESDMF	S69 SSTK	Qy 589 ANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT	Db 625 VSLSEIEEALAKNDVRSAE-IPVAQ-ETVVSET	Qy 649 TYKAPNGYTLEDLFATIKYYYEHPDERPHSN	Qy 705 ADEEPVEETPAEPEVPQVETEKVEA	Db 717 KDMSPLPESEVTLGKDVVILPETKVAEFNNV-T		Db 771 LAKNADLHSGTELIVDNSMAPASDLALPLET	RESULT 15 5231168-2	; Patent No. 5231168 ; APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; VUUST, JUNS; RIENECK, KLAUS; WIND, ANNETTE; JAKOB; TITLE OF INVENTION: MALARIA ANTIGEN	; NUMBER OF SEQUENCES: 19 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/409,658 ; FILING DATE: 18-SEP-1989 ; SEQ ID NO:2:	; LENGTH: 783 5231168-2 Query Match 3.5%; Score 146; D
	Db 5772 GVQQLANAKQQATQTVNGLNSLNDGQKRELNLLINSANTRTKVQEELNKATELNHAMEAL 5831	QY 429 KENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLER 473 ::	Qy 474 LNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVR-IAQ 519		Db 5949 TLDTAMLGLRKSIKDTKNSSKYINEDHDQQQAYDNAVNNAQQVIDETQATLS 6003	Qy         553 SHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKR 608           DD         6004SDTINQLANAVTQAKSNLHGDTKLQHDKDSAKQTIAQLQNLNSAQKH 6050	Qy 609IPLVRLPYMVEH	Db 6051 MEDSLIDNESTRTQVQHDLTEAQALDGLMGALKESIKDYTNIVSNGNYINAEPSKKQAYD 6110	6111 AAVQNAQNIINGTNQPTINKGNVTTATQTVVQYTKDALDGDHRLEEAKNNANQTIRNLSNL	Qy 662SATIKYYVEHPDERPHSNDGMGNASEHVLGKKDHSEDP 699	Db 6171 NNAQKDAEKNLVNSASTLEGVQQNLQTAQQLDNAMGELRQSI-AKKDQVKADSKYLNEDP 6229	QY 700 NKOFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVILAKVTDSSLKANATE 752  ON OTKONVORTETTINETONDELIZANTDAROGUMBEDALHGABETINDERGEP 6280	753 TLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKI 795	Db 6290 -LDGL-TDLTDAQREKLREQINTSNSRDDIKQKI 6321		US-09-513-783A-6 ; Sequence 6, Application US/09513783A ; Patent No. 6416959	; GENERAL INFORMATION:	TITLE DEPENDENCE: ASSISTANTION: A System for Cell Based Screening	FILE REFERENCE 97-02-11. CURRENT PELLING DATE: 2000-02-25 CURRENT FILING DATE: 2000-02-25	; NUMBER OF SEQ ID NOS: 180 ; SOFUMBE: Patentin Ver. 2.0 : SEO ID NO 6	TYPE: PRT	ORGANISM: Artificial Sequence PEATURE: OTHER INFORMATION: EYFP-DEAD-MAPKDM construct OTHER INFORMATION: EYFP-DEAD-MAPKDM construct	US-09-513-783A-6 Query Match Best Local Similarity 19.8%; Score 147; DB 4; Length 812; Matches 175; Conservative 103; Mismatches 331; Indels 274; Gaps 39;	VISHGDHYHYYNGKVPYDAIISEELLMKDP-NYKLKDE CFARYPDHMKQHDFFKSAMPEGYVQERIIFFKDDGNYKTRAEVKFE

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----AAAEA----- 210
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SYGMLPCDSF---ASTAVVSQEWSVGAPN 445
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3TEVVLATEVVLP-----666
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                                                                    ASDIIEDTGD------AYIVPHG 189
                                                                                                                                                                           IKRDFMAALEAEPYDDIVGETVEKTEFI 293
                                                                                                                                                                                                                   SAPETINITALISMNSNTNSOASOSNDIDS 269
                                                                                                                                                                                                                                                  SKP-TLLANGDHGMEGNNTAGSPTD--- 347
                                                                                                                                                                                                                                                                                          SRTARGVAVPHGDHYHFIPYSQMSELEER 326
                                                                                                                                                                                                                                                                                                                                                                SPGPOPAPNLKIDSNSSLVSQLVRKVGEG 386
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KDAAHADNVRTKEEINRQKQEHS----Q 141
                      : :: :| :: |
MADKQKNGIKVNFKIRHNIEDGSVQLAD 181
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|SALSKDPNEKRDHMVLLEFVTAAGITLG 233
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DTDQ---AEPFNEH-----RDDG 393
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ETKVATVPIKDK 811
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OBSEN, PALLE H.
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GENERAL INFORMATION:
APPLICANT: Lynn Dougette-Stamm et al
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BFIDERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BFIDERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
REIOR FILING DATE: 1997-08-14
REIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3159
LENGTH: 10182
                                                                                                                                     1971 ATNRVNAGLAQAIQNINNAHSTQEVNESKTNSIATIKSVQPNVIKKFTAINSLTQEANNQ 2030
                                                                                                                                                                                                                                                                                                       5650 LHTDQESTNRQIEGLSSLNTAQINAEKDLVNQAKTRTDVA-----QKLAAAKEINSAMS 5703
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596 AAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAP--
                                                                                                                                                                                                               1914 TE---REVNGAKTNGLEKINNIQPSTQTKTNAKQEINDKAQEQLIQINNTPDATEEEKQE
                                                                                          ---FATIKYYVEHPDERP---HSNDGWGNAS
                                                                                                                                                                                  687 EHVLGKKDHSEDPNKNF-----KADE--EPVEETPAEPEVPQVETEKVEA-----Q
                                                                                                                                                                                                                                                                             731 LKEAEVL----LAKVTDSSLKAN--AT------ETLAGLRINL----TLQIMD
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                                                                                                                                                                                                                                                                                                                                                                   768 NNSIMAEAEKLLALLKGSNPSSVSKEKI
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                                                                                          ·NGYTLEDL-
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Matches 189; Conserv
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                                                      GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO S.080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNQIDGIVSDGRQSINA---ITPDTSIKRNAKN--DIDIKAADKKIKIQRINDATDEEIQ 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1354 BANRKIE-----EAKIEAKDNIQRNSTRDQVNEAKTNGINKIENITPATIVKSEARQAVQ 1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -OGYVTSHGDHYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EPSPGPQPAPNLKIDSNSSLVSQL--VRKVGEGYVFEEKGISRYVFAKDLPSETVKNLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%; Score 163; DB 4; Length 3696; 18.5%; Pred. No. 0.0063;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 141; Mismatches 348;
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                   Sequence 5080, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-5080
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es 183; Conserv
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Steven C. Barash
Michael R. Pannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                 ----NTQSVAKGSTSKPANKSENLQSLLKELYDSPSAQRYSESDGLVFDPAKIISRTPNG 280
                                                     363
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                                                                                                                                                                                   340 -LTTSKELSSASDGYIFNPK-DIVBETATAYIVRHG--DHFHYIPK-----SNQIGQPT 389
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---EDGYGFDANRIIAEDES 431
PGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARG 303
                                                                                                        364 APNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSH 423
                                                     VAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQP
                                                                                                                                   ---PNEVVSSLGSLSSNPSS---
                                                                                                                                                               424 TLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTNKEK
                                                                                                                                                                                                                    484 LVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: < Unknown>
                                                                              281 VAIPHGDHYHFIPYSKLSALEEKIARMVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mark J. Hyman
RESISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 5235, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                     TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                           Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 886 amino acids
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SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Rockville STATE: Maryland
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                                                                                                                                                                                                                                                                   46 ITSQHQAQAABNINISDKISENQNNNATTIQPPKDTNQTQPATQP-----ANTAKNYPA-
                                                                                                                                                                                                                                                                                                                                             79 ISEELL----MKDPNYKLKDEDIVNEVKGGYVI----KVDGKYYVY--LKDAAHADNVRTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 EVELDINTASTWKKFEVYENNOKLPVRLVSYSPVPEDHAYIR---FPVSDGTQEL-KIVS
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                                                                                                                                                                                                                               21 IDGKQATQKTENL-TPDEVSKREGINAEQI-VIKITDQGYVTSHGDHYHYYNGKVPYDAI
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                                                                                                                                                                         246;
                                                                                                                 Length 886;
                                                                                                                                                                         Indels
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                                                                                                           4.1%; Score 169; DB 4; I
llarity 19.8%; Pred. No. 0.00022;
Conservative 138; Mismatches 343;
) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5235:
US-08-956-171E-5235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLKANATETLAGLRNNLTL-----
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                                                                                                              Query Match
Best Local Similarity
Matches 179; Conserva
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484 LVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGD 543
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------EDGYGFDANRIIAEDES 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNVRTKEEINROKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGDA 183
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                                                                                                                                                                                                                                                     Sequence 182, Application US/09536784

Patent No. 6573082

GENERAL INFORMATION:

GENERAL TOWN:

APPLICATT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452

CORRESPONDENCE ADDRESS:

ADDRESSER: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFFWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/536,784 FILING DATE: 30-Oct-1997 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
                                                 390 LPNNSLATPSP-SLPINPGTSHEKHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (301) 309-85
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                   :| | | :|: | 432 GFVMSHGDHNHYFFK 446
                                                                                                          544 AYVTPHMGHSHWIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                 US-09-536-784-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-536-784-182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 YIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSN 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVİKITDQGYVTSHG
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et. al.
N: Streptococcus pneumoniae Antigens and Vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                  Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 VAIPHGDHYHFIPYSKLSALEEKIARMVP
                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear / MOLECULE TYPE: protein US-08-961-083-182
                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                    STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                                                Maryland: USA
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 GPOPAPNIK-IDSN---SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKL
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                                                                                                                                                                                                                              49;
                                                                                                                                                                                                    63.6%; Score 2649.5; DB 4; Length 763; 66.8%; Pred. No. 2.3e-197; Live 77; Mismatches 132; Indels 49;
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                   SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
                                                                            INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                Best Local Similarity 66.8
Matches 519; Conservative
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Squence 6, Application US/09468656A

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Squence 6, Application US/09468656A

Squence 6, Application US/09468656A

Squence 6, Application US/09468656A

Squence 6, Application Userie 8.

APPLICANT: Johnson, Leslie 8.

TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus

TITLE OF INVENTION: Motify Naccine Group A and B Having Selected Structural

TITLE OF INVENTION: Motify 11 Present Application NUMBER: US/09/468,656A

CURRENT APPLICATION NUMBER: US/09/468,656A

CURRENT FILING DATE: 1999-12-02

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHADNVRTKEEINROKOEHSOHREGGTPRNDGAVALARSOGRYTTDDGYIFNASDIIEDT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 VSNPGTTNTINTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
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--EDGYGFDANRIIAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%; Score 1203.5; DB 4; Length 45.8%; Pred. No. 3e-85; ive 77; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPTLPNNSLATPSP-SLPINPGTSHEKHE
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; Sequence 182, Application US/08961083
: Patent No. 6159469
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus pneumoniae
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OY 120 AAHADNIKTKEEINROKQEHSOHREGGIPRNDGAVALARSOGRYTTDDGYIFNASDIIED 179  122 AAHADNIRTKEEIKROKQERSHNHNSRADNAVAARAQGRYTTDDGYIFNASDIIED 178  DD 122 AAHADNIRTKEEIKROKGERSHNHNSRADNAVAARAQGRYTTDDGYIFNASDIIED 178  QY 180 TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRONSDNTSRTNWVP 239  179 TGDAYIVPHGDHYHYIPKNELSASELAAAEAYNNGKQGSRPSSSSSYNA 227  QY 240 SVSNPGTTNTWTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHYESDGLIFDPAQITSR 299  10 SVSNPGTTNTWTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHYESDGLIFDPAQITSR 299  228 NPAQPRLSENHNLTVTPTYHQ-NGGBNISSLLRELYAKPLSERHVESDGLIFDPAQITSR 286  QY 300 TARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQFTPEPSP 359	Db 347 SPQPHPNPQPAPSHPIDEKI/WEAVHYGOGYPEENGGSRYTPARDLARHALPANGIDSKI 406  416 SKOESVSHTLTAKKENVAPRDQEFYDKAYNLITEAHKALPANKGRNSDFQALDKILERIN 475  Db 407 AKQESLSHKIGAKKTUDESSDFFYNKAYDLIARHQDLIDNKSRYODFBALDNILERIK 466  QY 476 DESTWERLYDDLIAFLAPITHPERLGKPNSOIETTEDEVALAQLADKYTSDSYIFDER 526  QY 477 DESTWERLYDDLIAFLAPITHPERLGKPNAQITTDDEIGVAKTYEDGYIFDER 526  QY 536 DIISDEGDAYVTPHMGHSHMIGKOSLSDEKKVAAQAYKEKGILPPSSDADVKANPTGDS 595  DIISDEGDAYVTPHMGHSHMIGKOSLSDEKKVAAQAYKEKGILPPSSDADVKANPTGDS 595  DIISDEGDAYVTPHMGHSHMIGKOSLSDEKKVAAQAYKEKGILPPSSDADVKANPTGDS 595  DIISDEGDAYVTPHMGHSHMIGNIARAAQAYAKEKGILPPSSDADVKANPTGDS 595  DJ 567 AAAITWNFVKEKILPLYRLPYWEHYVEHYKORGLIIPHYDHYHNIKFBWFDEGLYEAPKG 646  QY 558 AAAITWNFVKEKILPLYRLPYWEHYVEHYKORGLIIPHYDHYHNIKFBWFDEGLYEAPKG 646  QY 710 VBET	COMPUTER READABLE FORM:    COMPUTER READABLE FORM:   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33   COMPUTER: HP Vectra 486/33   OPERATING SYSTEM: MSDOS version 6.2   OPERATING SYSTEM: MSDOS version 6.2   APPLICATION NUMBER: US/09/536,784   FILING DATE: 30-Oct-1997   PRIOR APPLICATION: CURROWAPPERING APPLICATION NUMBER: US/09/51,083   FILING DATE: OCT-30-1997   ATTORNEY/AGENT INFORMATION:
QY         596 AAAIYNRVKGEKRIPLVKLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAMPDDHTYKAPNG 655           Db         607 AEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEMPDGLYEAPKG 666           QY         656 YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSE           QY         667 YTLEDLLATYKYVEHPDERPHSNDGRGNASEHVLGK	RESULT 6 Sequence 66, Application US/08961083 Setent No. 615346 GENERAL INFORMATION: APPLICATION: COLOI et al. TITLE OF INVENTION: Streptococcue pneumoniae Antigens and Vaccines NUMBER OF SEGUENCES: 452 CORRESPONDENCES: 453 COMPUTER: Diskette, 3.50 inch, 1.4Mb storage CONFUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: DIsket	Ouery Match 63.6%; Score 2649.5; DB 3; Length 763; Best Local Similarity 66.8%; Pred. No. 2.3e-197; Matches 519; Conservative 77; Mismatches 132; Indels 49; Gaps 8;  Qy 1 SYELGLYQARTV-KENNRVSYIDGRQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV 59

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119
724 PREEKPQSEKPESPKPTEEPEESPEESEEPQVETEKVEEKLREAEDLLGKIQDPIIKSNA 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 GPQPAPNLK-IDSN----SSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKL 415
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                                                                                                                                                                                                                               APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REFERENCE: 462201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILING DATE: 1998-12-21
SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 TSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYYYLKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.6%; Score 2772; DB 4; Length 8 65.0%; Pred. No. 7.8e-207; ive 91; Mismatches 144; Indels
                                       751 TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                              TYPE: PRT ORGANISM: Streptococcus pneumoniae
                                                                                                                                                      US-09-468-656A-4; Sequence 4, Application US/09468656A; Sequence 4, Application US/09468656A; Setent No. 6582706; GENERAL INFORMATION:
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Matches 541; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG------KQGSRPSSSSSYNA 246
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          APPLICANT: Johnson, Leslie S.
APPLICANT: Johnson, Leslie S.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FITLE OF INVENTION: Motifs
FILLE OF INVENTION: Motifs
FILLE OF INVENTION: MOTIFS
FILLE OF INVENTION: MOTIFS
FILLE OF INVENTION: MOTIFS
FILLE OF DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/113,048
PRIOR FILLING DATE: 1998-12-21
SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEEPSPQPTPEPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYELGRYQAGODKKESNRVAYIDGDQAGQKAENLTPDEVSKREGINAEQIVIKITDQGYV
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                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                            ; Score 2788.5; DB 4; Length
; Pred. No. 3.9e-208;
85; Mismatches 139; Indels
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Best Local Similarity 66.7%;
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Sequence 10, Application US/09468656A Patent No. 6582706
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver.
SEQ ID NO 8
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APPLICANT: Adamou, John E.
TITLE OF INVENTION: Vaccine Compositions Comprising Streptococcus
TITLE OF INVENTION: Pneumoniae Group A and B Having Selected Structural
TITLE OF INVENTION: Motifs
FILE REPERENCE: 469201-444
CURRENT APPLICATION NUMBER: US/09/468,656A
CURRENT FILING DATE: 1999-12-02
PRIOR PRILING DATE: 1999-12-21
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                               SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT
                                                                   SHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDA
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99.9%; Pred. No. 5.1e-315;
tive 0; Mismatches 1;
             TYPE: PRT ORGANISM: Streptococcus pneumoniae
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LENGTH: 819
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APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines WINDER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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100.0%; Pred. No. 4.9e-315;
tive 0; Mismatches 0;
              STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: IIC.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
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Best Local Similarity 100.
Marches 796; Conservative
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                                 481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                                                                                                                                             541 EGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
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100.0%; Pred. No. 4.9e-315;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-536-784-56
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TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/09536784 Patent No. 6573082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 796 amino acids
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STRANDEDNESS: single
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Best Local Similarity 100.
Matches 796; Conservative
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COUNTRY: USA
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US-09-561-818A-24

US-09-562-702A-28

US-09-561-818A-22

US-09-561-818A-22

US-09-561-818A-22

US-08-702A-26

US-08-702A-26

US-08-710-78A-22

US-09-513-783A-3

US-09-513-783A-3

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US-08-961-083-56
Sequence 56, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
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Sequence 182, App
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Sequence 5080, Ap
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1712.261 Million cell updates/sec
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-536-784-56

US-09-468-656A-10

US-09-468-656A-10

US-09-66-65A-4

US-09-66-65A-4

US-09-66-65A-6

US-09-536-784-182

US-09-66-1718-5235

US-09-134-001C-3159

US-09-134-001C-3159

US-09-134-001C-3159

US-09-541-783A-6

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US-09-513-783-6

US-09-513-783-6

US-09-513-783-6

US-09-513-783-6

US-09-513-783-6

US-09-513-82-6

US-09-513-83-118

US-09-50-650E-5

US-09-50-650E-5

US-09-200-650E-5

US-09-200-650E-5

US-09-200-650E-5

US-09-200-650E-5

US-09-200-650E-5

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US-09-200-650E-5
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US-09-562-702A-24
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Maximum Match 100%
Listing first 90 summaries
                                                                             protein search, using sw model
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4165
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No.
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95 Pp 95 Search completed: October 1, 2004, 07:16:43 Job time : 92 secs

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"Complete genome sequence of an M1 strain of Str
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001)
EMBL; AE006574; AAK34188.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 ERIARIIPLRYRSNHWVPDSRP-------
                                        InterPro; IPR001611; IRR.
InterPro; IPR001092; IRR SDS22.
InterPro; IPR0010437; Prok lipoprot S.
InterPro; IPR006270; Strep his triad.
Pfam; PF00560; IRR; 4.
Pfam; PF04270; strep his triad; 3.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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STRAIRS-SR30 / ArCC 700294 / Serotype M1;
MEDLINE-21192684; PubMed=11296296;
Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Ferretti J.J., Seate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
                                                                                                                                                                                                Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.B., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 TPNN------GVSAVDDGYVFNPNDIVRDTGDAYIVRHGDHYHYIPKSSLN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                       "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL, AE008464, AAK99714.1; -.
PIR; F97985; F97985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 243; DB 16; Length 182; 31.6%; Pred. No. 3.1e-06; Live 16; Mismatches 50; Indels 66
                                                                                                           Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome.
SEQUENCE 182 AA; 20145 MW; 29E12D653313A343 CRC64;
           Ol-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-UN-2003 (TrEMBLrel. 24, Last annotation update) Pneumococcal histidine triad protein B, truncation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                           Streptococcus pneumoniae (strain ATCC BAA-255 / R6)
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Pfam; PF04270; strep_his_triad; 2.
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MEDLINE=21429245; PubMed=11544234;
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Best Local Similarity 31.6%
Matches 61; Conservative
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                                                                                                                                        NCBI_TaxID=171101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 TYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPTDDGFILTKDSKILSKTDOG 89
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of Streptococcus pyogenes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 FLSGRGNLSNSRTYRRQNSDNTSRTNW--VPSVSNPGTTNTNTSNNSNTNSQASQSNDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVL---MLSDIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATANGI PGLHFPTSDGFQFNGQGIVGVTKDSILVDHDGHLHPISFADL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 5.4%; Score 223; DB 16; Length 792; sal Similarity 19.5%; Pred. No. 0.00032; 168; Conservative 116; Mismatches 279; Indels 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 KL--VD-----DLLAFLAP------ITHPERL-GKPN-----
                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 792 AA; 87458 MW; 9D5E32288485ACE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SLVSQLVRKVGEGY
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43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 YNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKD-----HYHNIKFAW-----FDDHT 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    487 TKINIGORTNPFORFGLSLMPNIEVL-GIGFTPINDMTPVLOFKKLKQLWMTNTGITDYS 545
                                                                                                                                                                                                                                                   QGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYV 115
                                                                                                                                                                                                                                                                                                                                                                            116 YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASD 175
                                                                                                                                                                                                                                                                                                                                                                                                            IIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWVPSVSNPGTTNTINTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQ 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 PHDDHTHVIMAKDI-----DLSKPIPNPH-------HDDEDHHKGHHHDES 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 AHKALFXNKGRNSDFQALDKLIERINDESTNKEKLVDD---LLAFLAPITHPERLGKPNS 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --IL---PPSPDADVKANP--TGDSAAAI 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DERPHSN-----DGWGNASEHVLGKKDHSE-DPNKNFKADEEPVEETPA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604 HINISDLTPLSNLTKLQELYLDHINIVKNLSA-LSGKKDLKVLDLSNNKSADESTLKTTSL 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 741 VTDSSLK----ANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKI 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- SVSKNKL 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----RKGGWGSIADRYQPQKKADS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 ETLLLNETNTSNLSFLKONPKVSNLTINNAKLASLDGIEESDEIVKVEAEGNQIKSLVLK 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SNGFLFNGRG 221
                                                                                                                                                                                  85
                                                                                                                                                                                  OEHKNSHHIKTKOVAKKKANKKKVSVKESHKKRRKOVAGVDFPTDDGFLLTKDSKILSHTD
                                                                                                                                                                                                                                                                                                              -- FYSDLKGSKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 QIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHW-----IGK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ETEKVEAQLKEAEVLLAK
                                                             Gaps
                                                                                                                           -NAEQIVIKITD
7.3%; Score 302; DB 16; Length 877;
20.8%; Pred. No. 1.4e-08;
.ive 95; Mismatches 263; Indels 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKV----
                                                                                                                           KENNRVSYIDGKOATOKTENLTPDEV----SKREGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 Y--KAP----NGYTLEDLFATIKY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 IKGTTPTGILVEHHNHLHFISFADL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DSLSDKEKVAAQAYTKEKG-
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56 QGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGIVVAHGNHSHFI-----FYSDLKGSKFS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPSPGPQPAPNLKIDSNSSLVSQLVRKV------GE-GYVFEEKGISRYVFA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGR 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GLHHPTSDGFLFNGQG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GAVAV-----NTLNDGYVFNPAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KENNRVSYIDGKQATQKTENLTPDEV---SKREGI------NAEQIVIKITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEHKNSHHİKTKÖVAKKKANKKKVSVKESHKKRKKVAGVDFPTDDGFLLTKDSKILSHPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWVPSVSNPGTTNTTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 İKGTİPTGILVEHHNHLHFİSF---ADLRKGGWGSİADRYQPQKKV-DSKKQSPS----
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 7.3%; Score 305; DB 16; Length 877; Local Similarity 21.3%; Pred. No. 9.3e-09; Loss 202; Conservative 95; Mismatches 272; Indels 380;
                                                                                                                                                                                                                                                      Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
MCBI_TaxIb=216495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                             877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00560; LRR; 3.
Pfam; PF04270; strep his triad; 4.
Hypothetical protein; Complete proteome.
SEOUENCE 877 AA; 97519 MW; C291DAFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; ALJ66848; CAD46577.1; -.
Sagalist; gbs0918; -.
InterPro; IPR001611; IRR.
InterPro; IPR001621; IRR SDS22.
InterPro; IPR005270; Strep_his_triad.
                                                                                                                                                                  Created)
                                                                                                                             PRT;
                   227 QNSDNTSRTNWVPSVS-NPG
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=NEM316 / Serotype III;
                                                                                                                                                                (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 25,
                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                       Hypothetical protein.
GBS0918.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                     01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunst F.;
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                                                                                                                             Q8E5R2
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                                                                                         RESULT 22
                                                                                                            Q8E5R2
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                                                                       220
                                                                                                                                                                                                                                                                                                                       380 LEATRWY-AEHRGHHIDALGKKDSTEKPKHISHEPNKEPHTEEEHHAVTPKDQRKGKPNS 438
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----QHREGGTPRNDGAVALARSQGRYTTDD 167
                                                                                                                                               ----TSNNSNTNSQASQS 264
                                                                                                                                                                                                                        324
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MEDLINE=21172873; PubMed=11274116;
MEDLINE=21172873; PubMed=11274116;
Granlund M., Michel F., Norghen M.;
Granlund M., Michel F., Norghen M.;
Intron identified in human isolates of group b streptococci.";
J. Bacteriol. 183:2560-2569(2001).
EMBL; AJ290522; CAC35985.1;
InterPro; IPRO06270; Strephis triad.
Pfam; PF04270; Strephis triad, 2.
TIGREMS; TIGRO1363; strephis_triad; 1.
                                                                                            81 YVTSHGDHYHFYNGKVPYDAIISEELLMTDBNYRFKQSDVINEILDGYVIKVNGNYYVYL
                                LKEGSKRINVRIKEQIQKQREEWSKGGSKGESGKHSSAKTQALSASVREAKASGRYTTDD
                                                                     GYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAF---LSGR-GNL---SN
                                                                                                                                                                      | : | : : | : : | SSSYIHASAPSGUVSTGRHANAP-ISIPRVTHANHWSKPAGNHATAPKHHAPTTKPINKD
                                                                                                                                                                                                                        NDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELE
                                                                                                                                                                                                                                            320 SALDKWLKRLYAQPLYARHVESDGLVYDPAQVNAFTAIGVSIPHGNHFHFIHYKDMSPLE
                                                                                                                                                                                                                                                                                                -PAPNLKIDSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SYELGLYQARTVKENNRVSYID----GKQATQKTENLTPDEVSKREGINAEQIVIKITDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKT-NKTMDQISAEEGISAEQIVVKITDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32043 MW; A15A8588EA8140E4 CRC64;
                                                                                                                                                                                                                                                                                              ERIARIIPLRYRSNH----WVPDS--RPEQPSPQPTPEPSPGPQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.3%; Score 679.5; DB 2;
53.8%; Pred. No. 2.2e-30;
tive 40; Mismatches 61;
                                                                                                                                                 SRIYRRONSD - - - - NISRINWVPSVSNPGIININ-
117 LKDAAHADNVRTKEEINRQKQEHS-
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Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus agalactiae.
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NON TER 289 28
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                                                                                                                                                                                                                                                                                                                                                                      374 SLV 376
                                                                                                                                                                                                                                                                                                                                                                                                           439 QIV 441
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Db 401 -ESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQ 444	CY 461 NSDFQALDKLIERINDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQL 520	TATA THE DESCRIPTION OF THE PROPERTY OF THE PR	Qy	Qy 581 PSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLJIPHKDHYHNI 640	Db 512 DKNHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIHVV 562	Qy 641 KFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGK 692	PGHEESGSVIPNVTPL	Qy 693 KDHSEDPNKNFKADEEPVEETPAEPEVPGVE- 723	Db 608 DKRAGMPNWQIIHSABEVQKALABGRFATPDGYIFDPRDVLAKETFVWKDGSFSIPRADG 667	Qy 724TEKVEAQLKEAEVLLAKYTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEA 775	776 EKILALLKGSNPSSVSKE 794 :	RESULT 20	93		DE Hypothetical protein.  GN GBS1925.  OS Streptococcus agalactiae (serotype III),  OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			MEDLIN Glaser Msadek	RT "Genome sequence of Streptococcus agalactiae, a pathogen causing RT invasive neonatal disease.";	RL MOI. Microbiol. 45:1499-1513(2002).  DR EMBL. AL76684; CAD47584.1;	DR InterPro; IPRO06270; Strep his triad. DR Pfam; PP04270; Strep_his_triad.	DR TIGRFAMS; TIGR01363; strep_his_triad; 1.  KW Hypothetical protein; Complete_proteome.  SQ SEQUENCE 481 AA; 53326 MW; DFDF0453D8A929BE CRC64;	Query Match 22.0%; Score 916.5; DB 16; Length 481; Rest Local Similarity 45,9%: Pred. No. 2.4e-43;	Matches 194; Conservative 73; Mismatches 105; Indels 51; Gaps	Qy	QY 57 GYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVY 116	DD 81 GYVISHGDHYHYYNGKVPYDAIISEELIMKDPSYVFNKADVINEVKDGYIIKVNGKYYLY 140
Db 633 VTPLDKRAGMPNWQIIHSAEEVQKALAEGRFAAPDGYIFDPRDVLAKETFVWKDGSFSIP 692	OY 721 QVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSI 771	693 KADGSSERTINASELSQRAEMEANANAGDALDIDAREE /3	QY       772 MAEAEKLIALLKGSNPSSVSKEK 794         :   :   .	RESULT 19	Q877X2 TD O877X2 PRELIMINARY: PRT: 794 AA.	027772; 027772; 01-TIN-2003 (TYEMBI.rel 24 Created)	01-00N-2003 (IIEMBLIEL 24, CIERCO 01-JUN-2003 (ITEMBLIEL 24, Last 01-OCT-2003 (TTEMBLEL 25, Last	Hypothetical protein.	Streptoccus pyogenes (serotype M3). Barteria. Firmicutes: Lactobarillales	rimirouces, Jacobaciiiaies, Streprococacea cous. D=198466;	SEQUENCE FROM N.A. STRAIN=SSI-1 / Serc Nakagawa I., Kuroka Yamazaki K., Okaha	Hayashi H., Hamada S.; "The genome of Sirvestve Streptococcus pyogenes of S. pyogenes Sir-1, SF370 and MGAS8232.";	Submitted (MAY-2002) EMBL; AP005146; BAC6	DR FINGEFEO; LFRUGGZ/U; Strep.nis_triad. DR Pfam; PF04270; strep_his_triad; 6. KW Hypothetical protein. SQ SEQUENCE 794 AA; 89290 MW; 9807269C8F5CB875 CRC64;	22.1%; Sc 30.0%; Pr vative 120;	Qy 14 ENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGBHYHYYN 70	Db 6 KDNQIAYIDDSKGKARAPKT-NKTMDQISAEBGISAEQIVVKITDQGYVTSHGDHYHFYN 64	Qy 71 GKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKYDGKYYVYLKDAAHADNVRTKE 130	131 EINRQKQEHSQH-REGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTGD :	125 QIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRGGRYTTDDGYIFSPTDIDDLGD 18	OY 103 AIVPHONINIENDEDANGEMEDS ORGENISMER RRQNDNISKINNY 239  Db 185 AYLVPHONIYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPGRRKAP-IP 241	240 SVS-NPGTININISNNSNINSQASQSNDIDSLLKQLYKLPLSQRHVE	Db 242 DVTPNPGGGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLDQLHRLDLKYRHVE 301 Ov 286 SDGIJVFDPAQITGRTARGVAVDHGHYHFIPYSQMSRIFRRIABITDIRVRSNHWVPDSR 345	302 EDGLIFEPTQVIXSNAFGYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQ 35	346 PEQPSPQPTPERSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGIS-RYVFAKDLP   :   : : : :	LL 1	

102; Martin S., Weber- Podbielski A.; ties to the LraI ad galactiae to human 9).  triad.  s triad. s triad. s triad.	SEQUENCE   82.2 AA; 92.386 MW; 80.54.51.5481.F98 CKC64;     Query Match	Db 81 YUTSHGDHYHFYNGKUPYDAIISEELLMTDENYHFKQSDVINEILDGYVIKUNGNYYYY 140  Qy 118 KDAAHADDVRTKEEINRQKQEHSQH-REGGTPRNDGAVALARSQGRYTTDDGY 169  141 KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNBAKRQGRYTTDDGY 200  170 IFNASDIIEDTGDAYIVDHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRR 226      :	QY         333 LRYRSNHWVPDSRPEQPSPGPAPNLKIDSNSSLVSQLVRKVGEGYVFEEK         392           I	
Db 81 YVTSHGDHYHPYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGGVIKVNGNYYYL 140  Qy 118 KDAAHADNVRTKEEINRQKQEHSQH-REGGTPRNDGAVALARSQGRYTTDDGY 169  141 KPGSKRKNIRTKQQIARQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY 200  170 IFNASDIIEDTGAVIVPHGAHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRR 226  Db 201 IFSPTDIIDDLGDAYIVPHGHHYHYIPKNDLSPSELAAAAWSQKQGRGARPSDYRP 258  Qy 227 QNSDHTSRTNWVPSVG-NPGTHNHYRYIPKNDLSPSELAAAQWSQCQRGARPSDYRP 258  Qy 227 QNSDHTSRTNWVPSVG-NPGTHNTNTSNNSNTNSQASQSNDIDSLLK 272  Db 259 TPAPGRRKAD-IPDVTPNPGGGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD 317	OY 273 OLYKLPLSORHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEBRIARIIP 332		Db 588 IHVVPYSWLTRNQIATIKYVWQHPEVRPDVWSKPGHEESGSVIPN 632  Qy 689 VLGKKDHSEDPNKNFKADEEPVEETPAEPEVP 720  Bb 633 VTPLDKRAGMPNWQIIHSAEEVQKALAEGRFAAPDGYIFDERDVLAKETFVWKDGSFSIP 692  Qy 721 QVETEKVBAQLEAKKNAGDATDTDKPEE 735  Db 693 RADGSSLRTINKSDLSQAEWQQAQELLAKKNAGDATDTDKPEE 735  Qy 772 MAEAEKLLALLKGSNPSSVSKE 794	RESULT 18 092HG7 ID 092HG7 AC 092HG7 DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 25, Last sequence update) DT 01-MAY-1999 (TrEMBLrel. 25, Last annotation update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DT 01-Cr-2003 (TrEMBLrel. 25, Last annotation update) DT 01-Cr-2003 (TrEMBLrel. 26, Last annotation update) DT 01-Cr-2003 (TrEMBLrel. 27, Last annotation update) DT 01-Cr-2003 (TrEMBLrel. 26, Last annotation update) DX Streptococcus agalactiae. OC Streptococcus agalactiae. OC Streptococcus OC

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508 IEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKV 567
                                                                                                                                                                                                                                                                                                           ----DKPKEKQQADK---SNENQQPSEASKEE 755
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Pfam; PF04270; strep_his_triad; 6.
IIGREAMs; TIGR01363; strep_his_triad; 1.
                           ----TKKVSRKVTKDGKV---
                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
                                                                                                                                        579 SFVÍPHIDHIHVVPYSWL----
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272; Conservative
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SEQUENCE 822 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 YVTSHGDHYHFYNGKVPFDAIISBELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 QNSDNTSRINWVPSVS-NPGTININTSN-----NSNTNSQASQSND-----IDSLLK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 DISDAYVFSK----ESIHSVD-----KGGVTAKHGDHFHYIGFGELEQYE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 -RYLAGO-----TEDNDSGSDHSKSSDKEVTHTFLGHRIKAYGKGLDGKPY 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 KALFXN----KGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SYELGLYQARTVKENNRVSYID---GKQATQKTENLIPDEVSKREGINAEQIVIKITDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSOGRYTTDDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY
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                                                                                                                                                                                                                         STRAIN=MGAS315 / Serotype M3;
MEDLINE=2213808; PubMed=12122206;
MEDLINE=2213808; PubMed=12122206;
Bares S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlibvert P.M., Musser J.M.,
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.6%; Score 940; DB 16; Length 823; Best Local Similarity 30.0%; Pred. No. 2.4e-44; Matches 262; Conservative 122; Mismatches 272; Indels 21.
                                                                                                                         SPYM3_1724.
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          823 AA; 92431 MW; 8C6CBD517A2DD616 CRC64;
                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Histidine triad protein.
                                                                                                                                                                                                                                                                                                                                            emergence.";
Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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                                        823 AA
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Pfam; PF04270; strep his triad; 6.
TIGRPAMs; TIGR01363; strep his triad; 1.
                                        PRT;
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                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 823 AA;
                                                                                                                                                                                 NCBI_TaxID=198466;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                      Streptococcus
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Q8K5Q1;
          RESULT 16
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-----GYIMPKDGKDYFYARDQLD----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VPQVE-----TBKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLT
                                                                       568 AAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNG
                                                                                                                                               ----IEPRLAVDVSSLPMHAGNATYDTGS
                                                                                                                                                                                                                    528 NLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGW----
                                                                                                                                                                                                                                                                                                                                                                                                                                    524 EESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFV
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29.5%; Pred. No. 3.6e-4%;
iive 98; Mismatches 235; Indels 318; Gaps
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Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 WKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKN----AGDATDT
                                                                                                                                                                                                                                                                                                                                                                ---GNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE----PE---
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Qy 452 KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQ 507	OY 508 IEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYUTPHMGHSHWIGKDSLSDKEKV 567	RESULT 14  10 08E4U1 10 06E4U1 11 DEBLIMINARY; PRT; 822 AA.  AC 08E4U1 11 OF 01-MAR-2003 (TERMBLEE]. 23, Created) DT 01-MAR-2003 (TERMBLEE]. 23, Last sequence update) DT 01-MAR-2003 (TERMBLEE]. 23, Last sequence update) DT 01-MAR-2003 (TERMBLEE]. 23, Last sequence update) DE Mypochetical protein.  COS STEPPCOCCOUS.  ON STEPPCOCCOUS.  ON NOTE TAXID=216495; RM 113 RM STREATHWENDER] 6 SECOTYPE III; RM MININE-22243508 PubMed-1215421; RM MASSIGN TO COUNTE N. Laliou! L., Poyart C., Trieu-Cuct P., RA MASSIGN ED P., RANDER FO.  RM MOLINE-22243508 PubMed-1215422]. RM MASSIGN TO COUNTE N. Laliou! L., Poyart C., Trieu-Cuct P., RA MASSIGN ED P., RANDER F.; RM MOLINE-22243508 PubMed-1215422]. RM MASSIGN TO COUNTE N. Laliou! L., Poyart C., Trieu-Cuct P., RA MASSIGN ED P., RANDER F.; RM MASSIGN ED PROMER AND TAXID TO COUNTE N. Laliou! L., Poyart C., Trieu-Cuct P., RA MASSIGN ED PROMER AND TAXID TO COUNTE N. Laliou! L., Poyart C., Trieu-Cuct P., RA MASSIGN ED P., RANDER F.; RM MASSIGN ED PROMER SECONDER
Qy 756 GLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEK 794  Db 733DKPKEKQQADKSNENQQPSEASKEE 757	RESULT 13  QBNZ82  DD QBNZ82  DD QBNZ82  DD COT-2002 (TrEMBLrel. 22, Created)  DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update)  DT 01-0CT-2002 (TrEMBLrel. 24, Last annotation update)  DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  DE Hypothetical protein spyMl8_2072.  GN SPYM18 2072.  OS Streptococcus pyogenes (serotype M18).  OC Streptococcus.  OX NCBI TaxID-186103;  RN   [1]  RN SEQUENCE FROM N.A.  SEQUENCE FROM N.	RT OWLEARAKE.  RY ARICH ACAG. SCI. U.S.A. 99:4668-4673(2002).  BY HEAL ABOUITOL AALOBS31.1.  BY HEAL ABOUITOL AALOBS31.1.  REAL ABOUTOLO AALOBS31.1.  REAL ABOUTOLO AALOBS31.1.  REAL ABOUTOLO AALOBS31.1.  REAL PROOFCATO. STREP INS TRIAG.  REAL PROOFCATO. STREP INS TRIAG.  REAL PROOFCATO. STREP INS TRIAG.  REAL PROOFCATO. STREP INS TRIAG.  SEQUENCE 823 AA, 92:85 M/; CORDETORCECOM.  SEQUENCE 823 AA, 92:85 M/; CORDETORCECOM.  REAL COCAL SIMILARILY COMPLETE PROCECURE 272; Indels 216; Gaps 29;  BEST LOCAL SIMILARILY 29.94; Bred. No. 1.16-44;  MATCHES 261, CONSETVATIVE 123; MISMATCHES 272; Indels 216; Gaps 29;  RYTSHCOHYHYTORRINAVSTIDCKCATORTELPPDVATREDINARDYNTITIOGS 57  1 SYELCIYOARTYKENNINYSTID SYGKARARATT.NKTMODISABGINARDYNTITIOGS 60  22 SYCLGKHMGPVTKUNQIAYIDDSKGKARARATT.NKTMODISABGINARDYNTITIOGS 80  SHIP YOTSHCOHHHYTORRINAVATICEELLAKEDBNYTLKEDEINAKEDRAYITORYL 140  BY YOTSHCOHHHYTORRINAVATICEELLAKEDBNYTLKEDEINAKEDRAYITORYL 140  CONSTRUCTION OF THE STREAM

RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";  RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  R EMEL, AROGGG23, AAX4688.1.;  R InterPro; IPRO06270; Strep his triad.  DR Pfam; PF04270; strep his triad.  R TIGREMAS; TIGR01363; strep his triad; difference in TIGR01363; strep his tr	Query Match 22.8%; Score 949; DB 16; Length 825; Best Local Similarity 29.5%; Pred. No. 7.7e-45; Matches 277; Conservative 100; Mismatches 214; Indels 348; Gaps 34; Ov 1 SYELGLYOARTWKENNRYSYIDGKOATOKTENLTPDEVSKREGINAEOIVIKITDOG 57		Db 81 YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDGYVIKVNGNYYYYL 140 Qy 118 KDAAHADNVRTKEEINRQKQEHSQH-REGGTPRNDGAVALARSOGRYTTDDGY 169	OY 170 IFNASDIIEDTGDAXIVPHGDHYHYIPKNELSASELAARAFLSGRGNLSNSKTYRR 226       :	259 TPAPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPRRNDASQNKHQRDEFKGKTFKELL. 272 KQLYKLPLSQRHYGSDGLVPDPAQITSRTARGVAVPHGDHYHPIPYSQMSELEBRIARII	Db 319 DQLHRLDLKYRHVEEDGLIFFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD 376 Qy 332 PLRYRSNHWVPDSRPEQPSPQPTPEPSPGPAPNLKIDSNSSLVSQLVRKVGEGYVFEE 391	Db 377RYLAGQTEDD 391  Qy 392 KGISRYVPAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLITEAH 451	Db 392IKAY	Db 413GKGLD 420  Qy 512 EDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAXVTPHMGHSHWIGKDSLSDKEKVAAQA 571	Db 421YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVAN 468 Qy 572 YTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLV	Db 469 WVKAKGQADELAALDQEGGKEK-PLFDTKKVSRKVTKDGKVGYNM 513 QY 619	Qy 629LIIPHKDHYHNIKFAWFDDHTYKAPNGYTL5DLFATIKYYVEHPDERPHSND 680 	QY 681 GWGNASEHVLGKKDHSEDENKNFKADEEEVEETPAEPE 718   1	QY 719VPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLA 755
OY 1 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVT 60	Db   142   AHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRYTTNDGSVYRNPADIIEDT 197   Oy	241 VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT 30	LEERIARIIPLRYRSNHWVPDS                   LEEKIARRVP VGEGYVFEEKGISRYVFAKDLP	Db 334 SGTGSTVSTNAK	SYIFDE       SYGFDA	QY 540 DEGDAVUTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTG-DSAAA 598 :: :     :     : :     : :     : :     : :     :   :     :     :   :     :   :     :   :     :   :     : :   :	Qy 599 IYNRVKGEKRIPLVRLPYMVBHTVEVKNGNLII-PHKDHYHNIKFA 643  Db 501 HEQDYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAIIYPHGDHHHADP 558	QY 644 WFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDP 699	Qy 700 NKNF 703  :   Db 611 NQNF 614	RESULT 12 Q99XV4 ID Q99XV4 PRELIMINARY: PRT: 825 AA.	Q99XV4; 01-UNA-2001 (TrEMBLrel. 17, Created) 01-UNA-2001 (TrEMBLrel. 17, Last sequence 01-UNA-2003 (TrEMBLrel. 24, Last annotati Hypothetical protein SPy2006.			RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., RA Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,

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                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pneumococcal histidine triad protein E precursor (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                    MEDINE=21101045; PubMed=11159990; Adamou JE., Hehintche J.H., Erwin A.L., Walsh W., Gayle T., Adamou JE., Hehintche J.H., Erwin A.L., Barren P., Lathigra R., Langermann S., Koenig S., Johnson S.; Barren P., Lathigra R., Indentification and characterization of a novel family of pneumococcal proteins (the Pht family) that are protective against sepsis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolnay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus
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                                                                                                                                                                                                                                   Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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40.9%; Pred. No. 2.5e-61;
iive 97; Mismatches 180;
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InterPro; JPR006270; Strep his triad.
Pfam, PF04270; Strep his triad; 6.
TigRN3163; Strep his triad; 4.
Signal; Hypothetical protein; Complete proteome.
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STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
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EMBL; AE007403; AAK75121.1;
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301 ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG 360
                                                                                                                                                                                                                                      421 VSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLNDESTN 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LTTSKELSSASDGYIFNPK-DIVEFTATAYIVRHG--DHFHYIPK-----SNQIG
                                                                                                                                                                                                                                                                                                                                                            481 KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
                                                                                                                                                                                                                                                                                                                                                                                                                    -----EDGYGFDANRIIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 EGDAYVTPHMGHSHWIGXDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PNEVVSSLGSLSSNPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VKGEKRIPLVRLPYMV--EHTVEVKNGNLII-PHKDHYHNIKFAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    502 EQDYPSNAKEMKDLDKKIEEKIAGIMKOYGVKRESIVVNKEKNAIIXPHGDHHHADP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 FDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDG----WGNASEHVLGKKDHSEDPN
                                                                                                                      POPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQES
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MEDLINE-1429245, PubMed=11544234;
HOSKINS J. Alborn W.B. Jr., Arnold J., Blaszczak L.C., Burgett S.

DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer Calinour K., Glass J.S., Khoja H., Kraff A.R., Jagace R.B.,

LeBlanc D.J., Lee L.M., Lefkowitz E.J., Lu J., Matsushima P.,

McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,

Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

Sun P.-M., Winkler M.B., Yang Y., Young-Bellido M., Zhao G.,

Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008464; AAK99712.1; -.
PIR; D97985; D97985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05CC226D2028F551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBDO07;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              29.8%; Score 1243; DB 16;
41.2%; Pred. No. 3.7e-61;
iive 94; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1039 AA
                               InterPro; IPR006270; Strep his triad.
Pfam; PF04270; strep his triad; 6.
TIGRFAMs; TIGR01363; strep_his_triad; 3.
                                                                                                                                                                              ----ISGTGSTVSTNAK----
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Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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TSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVDGKYYVYLKD 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLN 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||| : || || : ||| : |||| : || 366 SPQPAPNYIPAKDLSAETAAGIDSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724 TEKVEAQLKEAEVLLAKVTDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKK-----DHSEDPNK-----
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                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                   Length 853;
                                                                                                                                                                                                                      853 AA; 95225 MW; 9BF06A1EDE990CF5 CRC64;
                                                                                                                                                                                                                                                                                63.5%; Score 2733; DB 16; 63.5%; Pred. No. 1.1e-144;
                                                                                                                                                                                                                                                                                                                                            145;
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                                                                                                                                                                                                                                                                                                                                            92; Mismatches
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J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008464; AAK99711.1; -
PIR; C97985; C97985.
INTERPO: 1PR006270; Strep_his_triad.
Pfam; PF04270; Strep_his_triad.
TIGREAMS; TIGR01363; Strep_his_triad;
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846 ESQPTPI 852
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SEQUENCE 853 AA;
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   AAHADNIRTKEEIKRQKQEHSHNHGGGS--NDQAVVAARAQGRYTTDDGYIFNASDIIED
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                                                                TGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVP
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MEDLINE-2142245; PubMed=11544234;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S.,
DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Norris F.H., O'Gara M., Pery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pneumococcal histidine triad protein D.
                                                                                                      TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG---
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NCBI_TaxID=171101;
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65.0%; Pred. No. 7e-147;
ive 91; Mismatches 144;
                                         751 TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS 785
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Pfam; PF04270; strep_his_triad; 5.
TIGRPAMS; TIGR01363; strep_his_triad; 2.
Signal; Hypothetical protein; Complete proteome.
SIGNAL
                                                     AA.
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EMBL; AF318955; AAK06760.1;
EMBL; AE007403; AAK75120.1;
PIR; G95115; G95115.
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                                                                                                                                                                                                     Streptococcus pneumoniae
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839 AA;
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Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T.,
Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R.,
Langermann S., Koenig S., Johnson S.,
"Identification and characterization of a novel family of pneumococcal
                                                                                                                                                                                                                                                                                                                                                              TGDAYIVPHGDHYHYIPKNELSASELAAAEAYWNG-------KQGSRPSSSSYNA
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                                                                                                   proteins (the Pht family) that are protective against sepsis.";
Infect. Immun. 69:949-958(2001),
EMBL; AF318954; AAX06759.1; -.
                                                                                                                                                                                                                       2; Length 819;
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84; Mismatches 140; Indels
Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                 InterPro; IPR006270; Strep his triad.
Pfam; PF04270; strep his triad; 5.
TIGREAMS; TIGR01363; strep his triad; 2.
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pneumococcal histidine triad protein D precursor (Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE=21101045; PubMed=11159990; Adamou JE., Hethriche J.H., Erwin A.L., Walsh W., Gayle T., Adamou J.E., Hethriche J.H., Erwin A.L., Walsh W., Gayle T., Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R., Langermann S., Koenig S., Johnson S., "Identification and characterization of a novel family of pneumococcal proteins (the Pht family) that are protective against sepsis."; Infect. Immun. 69:949-958 (2001).
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Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey
Holt I.E., Loftus B.J., Vang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
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92228 MW; 43852B72E8163BDE CRC64;
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                                                                     EETPREEKPQSEKPESPKPTEEPEEESPEESPEESEEPQVETEKVKEKLREAEDLLGKIQ 811
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MEDLINE=21357209; Nelson K.E., Paulsen I.T., Bisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                  ANGVAVPHGDHYHFIPYSQLSPLEEKLARIIPLRYRSNHWVPDSRPEQPSPQSTPEPSPS
                                                                                                    KQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQALDKLLERLND
                                                                                                                KQESLSHKLGAKKTDLPSSDREFYNKAYDLLARIHQDLLDNKGRQVDFEALDNLERLKD
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Pfam, PF04270, strep his triad, 5.
TIGRFAMs, TIGR01363, strep his triad, 2.
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EMBL, AE007418; AAK75283.1; -.
PIR; B95136; B95136.
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FCC BAA-334 / TIGR4;
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                                                                                                                            SVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSR
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                                                                                                 SYELGLYQA-RTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYV
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       819;
                                                   47;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pneumococcal histidine triad protein B precursor (Fragment)
67.2%; Score 2797.5; DB 16; Length ilarity 67.0%; Pred. No. 2.5e-148; Conservative 84; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
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  EAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPKGY 680
                                                                                                                                                                                                       EETPREEKPQSEKPESPKPTEEPEESSPEESPEESEEPQVETEKVKEKLREAEDLLGKIQ 800
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                                                                               SLEDGLATVKYYVEHPNERPHSDNGFGNASDHVQRNKNGQADTNQTEKPNEEKPQTEKPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008479; AAK99864.1; -.
PIR; D98004; D98004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.4%; Score 3224; DB 16; Length 855; 75.0%; Pred. No. 3.6e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  855 AA; 96177 MW; 4350E82A3F97089A CRC64;
                                                                                                                                                                                                                                                           743 DSSLKANATETLAGLRNNLTLQIMDNNSIMAEAEKLLALLKGS
                                                                                                                                                                                                                                                                                          801 NPIIKSNAKETLTGLKNNLLFGTQDNNTIMAEAEKLLALLKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                855
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Pfam; PF04270; strep_his_triad; 5.
TIGRFAMs; TIGR01363; strep_his_triad;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created 01-MAR-2003 (TrEMBLrel. 23, Last se 01-OCT-2003 (TrEMBLrel. 25, Last an Histidine motif-containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=21246685; PubMed=11349048;
Zhang Y., Masi A.W., Barniak V., Mountzouros K., Hostetter M.K.,
Green B.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from Streptococcus pneumoniae, Protects Mice against Intranasal Pheumococcal Challenge.";
Infect. Immun. 6932-1836(2001).
EMBL, AR340221, AAX26659.1; -.
InterPro; IPR006270; Strep his triad.
Pfam; PF04270; strep—his triad.
Figh, PF04270; strep—his triad.
FIGRFAMS; TIGR01863; strep his triad.
SEQUENCE 844 AA; 94769 \( \text{MW}, \) D738A55290FF8902 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           'Recombinant PhpA Protein, a Unique Histidine Motif-Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 844;
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                                                                                                                                                                                                       Streptococcus pneumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.7%; Score 3236; DB 2; 75.3%; Pred. No. 7.5e-173; tive 66; Mismatches 99;
                        844 AA
                                                                            Created)
                                                                    (TrEMBLrel. 17, C (TrEMBLrel. 17, L (TrEMBLrel. 24, L
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                        PRELIMINARY;
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                                                                                                                                                                                                                                                           Streptococcus
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01-JUN-2003
                                                                         L-JUN-2001
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                                                                                                                                                                                                                                                                          GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                                                                                                                                                                                                                         0
                                                                                                                                                                                     Length 828;
            "Genome of the bacterium Streptococcus pneumoniae strain R6.
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008479; AKY99865.1; -.
PIR; E98004, E98000.
PIR; E98004, E98000.
PIREPRO; IPR006270; Strep_his_triad.
PEGM; PF04270; strep_his_triad.
TIGREMMS; TIGR01363; strep_his_triad; 2.
                                                                                                                                                                                                                       Indels
                                                                                                                                                       828 AA; 93015 MW; 12CCCF407B550C1D CRC64;
                                                                                                                                                                                     99.9%; Score 4159; DB 16; 99.7%; Pred. No. 1.6e-224; iive 0; Mismatches 2;
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Matches 794; Conservative
                                                                                                                                   Complete proteome. SEQUENCE 828 AA;
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                                                                                       GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRIYRRQNSDNISRINWVPS
                                                                                                                                     VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                          VSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVESDGLVFDPAQITSRT
                                                                                                                                                                                                         ARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPSPG
                                                                                                                                                                                                                          ARGVAVPHGDHYHFIPYSQMSELEERIARIIDIRYRSNHWVPDSRPEQPSPQPTPEPSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21429245; PubMed=11544234; Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P. M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
AHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT
                                                                 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pneumococcal histidine triad protein A.
PHTA OR SPR1061.
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NCBI_TaxID=171101;
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                                                                                 127 VSHTLITAKKENVAPRDQEFYDKAYNLLITEAHKALFENKGRNSDFQALDKLLERLNDESTN
                                                                                                                            KEKLVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISD
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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0; Mismatches 0;
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    Q9nyf8 homo sapien
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Pred. No. 9e-225;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                              ALIGNMENTS
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Pfam; PF04270; strep_his_triad; 5.
TIGRFAMs; TIGR01363; strep_his_triad; 2.
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MEDLINE=21357209; PubMed=11463916;
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EMBL; AE007418; AAK75284.1; -.
PIR; C95136; C95136.
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Matches 795; Conservative
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SEQUENCE F
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Q9veu8 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine + phosphate.
-!- SUBUNIT: The carbonic-anhydrase like domain binds to contactin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Sepecifically expressed in the central nervous system, where it is localized in the Purkinje cell layer of the cerebellum, the dentate gyrus, and the subependymal layer of the anterior horn of the lateral ventricle. Developmentally regulated
                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 87:7000-7004(1990).
-!- FUNCTION: May be involved in the regulation of specific developmental processes in the CNS.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: Contains 1 eukaryotic-type carbonic anhydrase domain.
-:- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
-:- SIMILARITY: Contains 1 fibronectin type III domain.
-:- CAUTION: Called RPTPAse beta in Ref.2 and Ref.4.
                                                                                                                                                                                                                                                                                                       family of receptor-linked protein-tyrosine-phosphatases expressed in
                                                                                                                                     human receptor-like protein
                                                                                                                                                                                                                 TISSUE=Brain stem, MEDLINE=90384936; PubMed=2169617; MEDLINE=90384936; PubMed=2169617; Mayblan R., Morse B., Huebner K., Croce C., Howk R., Ravera M., Ricca G., Jaye M., Schlessinger J., "Cloning of three human tyrosine phosphatases reveals a multigene
"The cloning of a receptor-type protein tyrosine phosphatase expressed in the central nervous system."; J. Biol. Chem. 268:10573-10581(1993).
                                                                                                                                                                                                     SEQUENCE OF 1749-1990 AND 2047-2280 FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
                                                                  SEQUENCE OF 1479-2091 FROM N.A. (ISOFORM LONG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P23471-2; Sequence=VSP_005151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P23471-1; Sequence=Displayed;
                                                                                                                    Krueger N.X., Streuli M., Saito H.; "Structural diversity and evolution of tyrosine phosphatases."; EMBO J. 9:3241-3252(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00134; carb anhydrase; 1. Pfam; PF00104; fn3; 1. Pfam; PF00102; Y phosphatase; 2. PRINTS; PR00100; PRTYPHPHTASE. Probom; PD000865; Euk Coanhd; 1. SMART; SM00060; FN3; 1.
                                                                                                  MEDLINE=91006018; PubMed=2170109;
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O-LINKED (XYL. . .) (CHONDROITIN SULFATE)
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                                                                                      BY SIMILARITY.
RECEPTOR-TYPE PROTEIN-TYROSINE
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SMART; SM00194; PTPC; 2.
PROSTIE; PS00183; TYR_POSPHATASE 1; 1.
PROSTIE; PS50056; TYR_PHOSPHATASE 2; 2.
PROSTIE; PS50055; TYR_PHOSPHATASE_PTP; 2.
Signal; Glycoprotein; Transmembrane; Hydrolase; Repeat; Alternative splicing.
1 24 BY SIMILARITY.
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1178 DSK 278 PLS 1238 QLA 325 ERLI 1288 KLI	TOGESSLSSDIYKLKFEASEBRÜKSLESKLSKUES  -FYDKAYNLLTEAHKALFXNKGRNSDF	Db 1499LRÉHIHALKQAEEDVKNMASIIEKLKTÖNKQKEKLIWERE 1538  Qy 581 -PSPDADVKANPTGDSAAIYNRVKGEKRIPLVRLPYWVEHTVEVKNGNLIIPHKDHYHN 639  [	QY         700 NKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKV	SUL	Demographen (Institution of Burkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL TaxID=9606;  NCBL TaxID=9606;  NI
F-1 F1	PRINIT (IN	NI)	SSTIKQOKQOFENCMDDLQG MASIIEKLKTQNKQKEKLIW > P (IN REF. 1). SEAARSLYKSGGNVD (IN NGTKFKEW (IN REF.		COLD   COLD   COLD
	NESLINRWISSETLO -> RIAIKILKPAINIT REF. 1) DDLUSE -> MTLFL (IN REF. 1) AQN -> RKI (IN REF. 1). S -> C (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> D (IN REF. 1). C -> C (IN R	V (IN REF. 1). LNKRISG -> LNKRISG -> REF. 1). REF. 1). REF. 1). REF. 1). MLE -> LTKG	D -> H (IN REF. 1).  SEQLDRLQKDLESTERQKELLSSTIKQQKQQFENCMDDLQG SEQLDRLQKDLESTERQKELLSSTIKQQKQQFENCMDDLQG NELREHIHALKQAEDVKUMASIIEKLKTONKQKEKLIW EREMERNDSDMQLQETLLE -> P (IN REF. 1). D -> V (IN REF. 1). DLLKQLDHYTKVVEMLN -> SEARSLYKSGGNVD (IN REF. 1). MISSING (IN REF. 1). MISSING (IN REF. 1).	FDDE -> LMM (IN REF. 1).   D -> E (IN REF. 1).   S -> D (IN REF. 1).   S -> D (IN REF. 1).   S -> W (IN REF. 1).   FWK -> NGGRRLDADDL (IN REF. WW; 6F54C7611F43DC9F CRC64   SCORT 141.5; DB 1; Lengt   Sted. NO. 10;   Sted.	TPDEVSKREGINA-
695 736 742 756 756 773 793 794 896 900 900 900 911	. 4-10000000004.0 4-111111111		4400 1400 454 1554 568 1568 630 1646 698 1704 725 1737	1757 1777 1788 1825 1904 ; 22363	KENNRVSYIDGKQATQKTENLTPDEV-
	COMPLICT 913 COMPLICT 93 COMPLICT 95 COMPLICT 100 COMPLICT 100 COMPLICT 106 COMPLICT 106 COMPLICT 108 COMPLICT 112 COMPLICT 113 COMPLICT 114	инна анна	CONFLICT 146 CONFLICT 156 CONFLICT 165 CONFLICT 165		13 13 998 56 052 104 104 1130
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STRAIN=S288c / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | :: :: | | :: : | | :: | | :: | | TVSS---NKDDVMVNSGARELPMPLHQQQYIXP----YYQYTSNNNNVTA-----
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MEDLINE=91088308; PubMed=2263482;
Sweeney F.P., Watts F.Z., Pocklington M.J., Orr E.;
"The MYO1 gene from Saccharomyces cerevisiae: its complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Mismatches 118; Indels 111; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SPQPTPEPSPGPQPAPNLKIDSNSSLVSQLV 380
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                 3.4%; Score 141.5; DB 1; Length 490; 19.3%; Pred. No. 1.5;
                           repressor activity; IDA.
                                                                                                                                                                                                                                                                                                                                                            4D0DA8DE43F171ED CRC64;
GO, GO:0003677; F:DNA binding; IPI.

GO; GO:0016564; F:transcriptional repressor activity
GO; GO:0006350; P:transcription; IGI.

GO; GO:0006350; P:C242;
PEam; PF00096; zf-C2H2; \(\frac{7}{2}\)

FAM; PF00096; zf-C2H2; \(\frac{7}{2}\)

FAM; PF00096; zf-C2H2; \(\frac{7}{2}\)

FROSITE; PS00028; ZINC FINGER C2H2 1; I.

PROSITE; PS00028; ZINC FINGER C2H2 2; I.

Nuclear protein; Zinc-Finger; Metal-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 QSNDIDSLLKQLYKLPLSQRHV--ESDGLVFDPAQITSR--
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01-FEB-1995 (Rel. 31, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
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C2H2-TYPE 2.
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Nucleic Acids Res. 18:7147-7147(1990)
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MYO1 OR YHR023W.
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Best Local Similarity
Matches 68; Conserv
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P08964;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watts F.Z., Shiels G., Orr E.; "The yeast MYO1 gene encoding a myosin-like protein required for cell
MEDLINE=94378003; PubMed=8091229; Johnston T., Ding H., Dover J., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Lou Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y., Latrefile P., Louis B.J., Macri C., Mardis B., Menezes S., Mouser L., Mhan M., Rifkin L., Riles L., St Perer H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Materston R., Wilson R.,
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                                                                                                                                                                                                                                                                    "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
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V -> S (IN REF. 1 AND 3).
L -> F (IN REF. 1 AND 3).
L -> S (IN REF. 1).
MISSING (IN REF. 1).
N -> S (IN REF. 1 AND 3).
QQAKFI -> TKLESL (IN REF. 1).
D -> S (IN REF. 1).
SKGPPTG -> ARGHDR (IN REF. 1).
D -> V (IN REF. 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN REF. 3).
EKSSSA -> GKNLLVC (IN REF. 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53947; CAA37894.1; -.
EMBL; X06187; CAA29550.1; -.
EMBL; V10399; AAB68872.1; -.
PIR, S46773; S46773.
HSSP; P08799; HMND.
Germonline; 139340; -.
SGD; S0001065; MYO.
GO; GO:0000142; C:contractile ring (sensu Saccharomyces); IDA.
GO; GO:000010; P:axial budding; IMP.
GO; GO:000010; P:axial budding; IMP.
GO; GO:000010; P:response to osmotic stress; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Required for cell division.
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
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InterPro; IPR0010048; Myosin, head.
InterPro; IPR0010093; Myosin, head.
PRINTS; PR00103; MYOSINHEAVY.
ProDom; PR00103; Myosin, head; 1.
SMART; SM0015; IQ; 1.
SMART; SM00242; MYSc; 1.
SMART; SR50096; IQ; 1.
Myosin; Actin-binding; ATP-binding; Coiled coil.
INTERPORATION ACTIN-binding; ATP-binding; LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TD -> LM (IN REF. 1).
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-> D (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88111539; PubMed=3322809;
                                                                                                                                                                                                                                                                                                                                      Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-760 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LNDESTNKEKLVDDLL-AFLAPITHPERLGKPNS 506
                                                                                                                                                                                                                                                   QIEYTEDEVRIAQL-----ADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKD
                                                                                                                                                              --EKIEIQOT
                                                                                                                                                                                                                                                                                                                                                                                                                                      673 DERPHSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEET---PAEPEVPQVETEKVEA
                                                                                                                                                                                                                    560 SLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRI-PLVRLPYMV
                                                                                                                                                                                                                                                                                                                          EHTVEVK--NGNLIPHKDHYHNIKFA----WFDDHTYKAPNGYTLEDLFATIKYYVEHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97313268; PubMed=9169872; Brown D., Chillingworth T., Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madison J., Winston F.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 387:90-93(1997).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
                                                                                                                                             (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc finger protein MOT3/HMS1.
MOT3 OR HMS1 OR YMR070W OR YM9916.09.
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TRANSFAC; T03448; -.
TRANSFAC; T03500; -.
SGD; S0004674; MOT3.
GO; GO:0005634; C:nucleus; IDA.
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  ---KLLER-
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STRAIN=S288C / AB972;
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10-OCT-2003
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P54785;
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                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                               TISSUE SPECIFICITY: GROWTH CONES OF EMBRYONIC VERTEBRATE NEURONS.
DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST
                                                           DEVELOPMENTAL STAGE: IS EXPRESSED IN THE NEURULA AND PERSIST DURING EMBRYOGENESIS IN THE BRAIN, CRANIAL NERVES, AND SPINAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1744;
                                                                                                                                          SIMILARITY: Belongs to the intermediate filament family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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LINKER 1.
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COIL 2B.
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Pfam; PF000038; filament; 1.
PROSITE; PS00226; IF; I.
Intermediate filament; Coiled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                    269 SSGSGFSSGGSGNPRKNLFSPYLPQSSIPAL---LAERRLVTGILIVSKKN----RSDAFV 322
                                                                                                                                                                        SVDG---LDAEVFICGSKDRNRALEGDVVAIELLDVDEVWAGKLEKEENRRRKDPISTRG 379
212 RNLDAQWRPSSLSQTNSPTHAANPSFPGTIVTHNTSNFRPEGGGHRHRRSTGSL---SVG 268
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                                                                                                                                                                                                                    484 LVDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGD
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                                                                                                                                                                                                                                                                                                             544 AYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVK-----ANPTG
                                                                                                                                                                                                                                                                                                                                         427 KYA----GH------VVAVLQRAPGQVFSGTLGTLRPSSAANKERQTSSGNQGSSNNSG
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                                       382 KVGEGYVFEEKGISR-YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFY
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                                                                                                                                441 DKAYNLLTEAHKALFXNKGRN----SDFQALDKL-----LERLNDESTNKEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agarwal A., Sloger M.S., Oyama M., Blumberg D.D., "Analysis of a novel cyclic Amp inducible prespore gene in Dictyostelium discoideum: evidence for different patterns of CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70
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13BA634CCE7AA502 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cAMP-inducible prespore protein D7 precursor
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Differentiation 57:151-162(1994)
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95343 MW;
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                                                                  DNVRTKEEIN--RQKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YHFIPYS 318
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LGEVKHDSLRDSATNYIWGLLDKIQSYLPKDNNKVSKVEEAFSSGQNNNIGSSIGDSTGA
                                                                                                                  STSPQFQSINGLSGASQSSGSSTGGTGDSDSK-----TTNEALIFSSKVSTTDRQ
                                                                                                                                                                                                              DAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEHTVEVKNGNLI I PHKDHYHNI KFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 LVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQE
                                                                                                                                                                                                                                                                                                                                                      SNNSNTNSQASQSNDIDSLLKQLYKLPLSQRH-
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Tadpole head;
MEDLINE=92398961; PubMed=1524825;
Hemmati-Brivanlou A., Mann R.W., Harland R.M.;
Hemstipersesed in the growth cones of embryonic vertebrate neurons defines a new class of intermediate filament protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---bkeqlidiqnrepgiyknq---Odlk------Qekranqqeli----
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
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--FDPAQITSRTARGVA-VPHGDHYHFIPYSQMSELEERIARIIPLRYR 336
                                                                                                                                                                                                                                                                                              451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 KVAAQAYTKEKGILPPSPDADVKA-----NPTGDSAAAIYNRVKGEKRIPLVRLPY 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KADEEPVEETPAEPEVPQVETEKVEA 729
-NPGTININISNN 254
                                                                                                                                                                                                                                                                                              397 YVFAKDLPSETVKNLESK---LSKQESVSHTLTAKKENVAPRDQEFYD--KAYNLLTEAH
                                                                                                                                                                                                                                                                                                                                 528 EAQYEDL----VKKLEAKNIEISQISGKEQSLTEKNENLSNELKKVQDQLEKLNNLNITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IQIKPVRG
                                  EEMIKSIENPPSEDKAHHLLQFNKPEERVHDLPEKKLQKHFDVAKDTLNVGLRNTTVELS
                                                                                                           SNTETMLKQQYEDIKENLEQKMSSSKDEMAKTINELSVTQKGLIMGVQEELLTSSGNIQT
                                                                                                                                                                                 456 ALVSEMNNTROELLDDA---SOTAKNYASLENLVKAYKAEIVOSNEYEERIKHLESER--
                                                                                                                                                                                                                     337 SNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEKGISR
                                                                                                                                                                                                                                                                                                                                                                      KALFXNK--GRNSDFQAL----DKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPN
                                                                                                                                                                                                                                                                                                                                                                                                      584 KSNYENKISSONEIVKALVSENDTLKORIQOLVEIKENEOKD-----HTTKLEAFOKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                             SQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TL-----KOQVÍVLKSEKQDITAEKLELQDNLESLEEVTKNLQQKVQSQKR----ELEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 MVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The fission yeast sts5+ gene is required for maintenance of growth polarity and functionally interacts with protein kinase C and an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
MEDILE=9704172; PubMed=8886983;
Toda T., Niwa H., Nama H., Dhut S., Eddison M., Matsusaka T.,
Yanagida M., Hirata D.;
                                                                                                                                                                                                                                                        ----STLSSQKNQIISSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKVD------HISKSRINSSKETSKFNDEFDLSSSSNDDLELTNPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                         NSQASQSNDIDSLLKQLYKLPLSQRH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STS5_SCHPO STANDARD; PRT; 1066 AA. 074454, 010452, 10466-CT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003_(Rel. 41, Last annotation update)
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MEDLINE=21848401; PubMed=11859360;
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J. Cell Sci. 109:2331-2342(1996)
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STS5 OR SPCC16C4.09.
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NCBI_TaxID=4896;
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TNWVPSVS-
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RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Rajendream M.A., Davis Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronis, A., Davis P., Feltwell T., Fraser A., Ra Collins M., Connor R., Cronis D., Hadlingworth T., Churcher C.M., RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Hucher E.J., Hunt S., Jagels K., James K., Jones M., Leather S., McDonald S., McLean J., RA Money P., Molle S., Pearson D. Quail M.A., Rabbinowitsch E., Rolliver K., O'Neil S., Pearson D., Quail M.A., Stevens K., Stevens K., Anylor K., Taylor R., Rauders D., Seeger K., Sharp S., Raplor K., Taylor K., Taylor R., Ranstreels E., Rieger N., Schaefer M., Mchlert H., Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Whitehead S., Weltjens I., Wanstreels E., Rieger M., Schaefer M., Mchler H., Rabut S., Rabel C., Fuchs M., Fritzc C., Holzer E., Mosell D., Hilbert H., Rabut S., Lehaue V., Mortier S., Rabel C., Puchs M., Wedler H., Rambut R., Purnelle B., Radibert F., Aves S.J., Xiang Z., Huut C., Moore K., Hurst S.M., Lowe T., Jimenen S., Gloux S., Lelaure V., Mottier S., Lowe T., Jimenen S., Gloux S., Lelaure V., Mottier S., Lowe T., Worceno S., Armstrong J., Forsburg S.L., Radibert F., Aves S.J., Jimenen S., Gloux S., Lelaure V., Mottier S., Radibert F., Aves S.J., Jimenen S., Gloux S., Lelaure V., Mottier S., Lowe T., Moreno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Radibert E., Moseno S., Armstrong J., Forsburg S.L., Lander M., Radibert E., Moseno S., Armstrong J., Potashkin J., Stepankin J., Stepankin J., Stepankin J., Stepankin J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ORHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELE--ERIARIIPL 333
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V -> G (IN REF. 1).
W; 077187800B330C15 CRC64;
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Pred. No. 4;
9; Mismatches 192;
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PROSITE; PS01175; RIBONUCLEASE_II; FALSE_NEG
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InterPro; IPR001900; Ribonuclease_II.
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CONFLICT 5 5 F ->
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Best Local Similarity 21.94
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        699 PNKNFKADEEPVEETPAEPE--VPQVETEKVEAQLKEAE-----VLLAKVTDSSLKANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               710 INNYLKAENQKLIQLKSELEKVLSLIDSSIFKVELKELQQRLDKFILPEKITQ----LRDA
                                                                                                                                                                                                                                                                                                  KIDSNSSLVSQLVR-----KVGEGYVFEEKGISRYVFAKD-----LPSETVK----
                                                                                                                                                                                                                                                                                                                                                 ---NLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFXNKGRNSDFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 GSFKLNDQVTLSHDETWRKLAANNHSLEHLLHAALQKEIDPLIKQSGAFKSAQKATIDFN
                                                                               TIGRFAMs; TIGR00344; alas; 1.
PROSITE; PS50860; AA TRNA LIGASE II ALA; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Synaptonemal complex protein ZIP1.
ZIP1 OR YDR255W OR D9819.9.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                               159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       751 TETLAGLRNNLTLQIMDNNSIMAEA-----EKLLALLKGSNPSSV 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDTLLALKNDINQLKTKNYKVSQQALALSIKKQLLSLVDENKSYV 811
                                                                                                                                                                               Indels
                                                                                                                                                        Length
                                                                                                                               900 AA; 104301 MW; AA54520BFB3949A2 CRC64;
                                                                                                                                                     / Match 3.4%; Score 143.5; DB 1;
Local Similarity 19.7%; Pred. No. 2.8;
hes 127; Conservative 109; Mismatches 250;
                                                                                                                                                                                                                                                    RII----PLRYRSNHWVPDSRPEQPSPQPTPEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          875 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               664 FGDYSVELCGGTHVANTASIEDCFITDFYSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVKGEKRIPLVRLPYMVEHTVEVKNG-
                    HAMAP; MF_00036; -; 1.
InterPro; IRR002318; tRNA-synt_2c.
InterPro; IPR006193; tRNA-synt_Ala.
Pfam; PF01411; tRNA-synt_2c; 1.
PRINTS; PR00980; TRNASYNTHALA.
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C64232; C64232.
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SEQUENCE 900 AA
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P31111;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
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                                                                                                                                                                                                                                                                                                                                                                          Favello A., Fulton L., Gattung S., Greco T., Kirsten J.,
Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
Johnson D., Johnston L., Langston Y., Latreille F., Le T.,
Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D.,
Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for meiotic chromosome synapsis and cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 ----KDPNYKLK------DEDIVNEVKGGYVIKVDGKYYVYLKD------AAHADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ELGLYQART-VKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 LQKQQQDNAKLKVRLQSYASNSDKINE-----KV-GKYKSCLETLQERIATLTSHKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 VRTKEEINROKQEHSQHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FKTS---IENLNKTINDLGKNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQNSD-----NTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               progression. May act as a molecular zipper to bring homologous chromosomes in close apposition. ZIP1 may encode the transverse filaments of the synaptonemal complex. -:- SUBCELLULAR LOCATION: SYNAPSED MEIOTIC CHROMOSOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 875;
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                                                                                                                                                       ., Engebrecht J.A., Roeder G.S.; is a synaptonemal complex protein required for meiotic
                                                                                                                                                                                                                                                                                                                                                      Cooper J., Ding H.,
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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GO; GO:0007126; P:matlosis; IMP.
GO; GO:0007129; P:synaptsis; IMP.
Nuclear protein; Meiosis; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> A (IN REF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 142.5;
Pred. No. 3:
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                                                                                                                                                                                                                                                                                                                         STRAIN=S288c / AB972;
Johnston M., Andrews S., Brinkman R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 EADAELMKKGKEIEYL-KRELDDCS---
                                                                                                      STRAIN=BR1824-3B;
MEDLINE=93161412; PubMed=7916652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 T
100035 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L06487; AAA35239.1; -. EMBL; U51031; AAB64474.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S70115; S70115.
GermOnline; 140777; -.
                                                                                                                                                                                                                chromosome synapsis."
Cell 72:365-378(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0002693; ZIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
55
875 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 HGD-----
                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
CONFLICT
SEQUENCE
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DOMAIN
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41;

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SEQUENCE FROM N.A. (ISOFORM 1C), SUBCELLULAR LOCATION, AND INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS IC AND 3A), FUNCTION, INDUCTION, TISSUE SPECIFICITY, SUBCELLULAR LOCATION, PHOSPHORYLATION, MUTAGENESIS OF ARG-205; PRO-206; THR-207; SER-208; LEU-209; THR-266; THR-276 AND THR-287, AND INTERACTION WITH MAPK81P2; MAPK8; MAPK9; MAPK10; MAPZK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20560743; PubMed=11106729; Bowman A.B., Kamal A., Ritchings B.W., Philp A.V., McGrail M., Gindhart J.G., Goldstein L.S.B.; "Kinesin-dependent axonal transport is mediated by the Sunday Driver
                                                                                                                                                                                                                                          Ito M., Yoshioka K., Akechi M., Yamashita S., Takamatsu N., Sugiyama K., Hibi M., Nakabeppu Y., Shiba T., Yamamoto K.-I.; "JSAPI, a novel jun N-terminal protein kinase (JNK)-binding protein that functions as a scaffold factor in the JNK signaling pathway."; Mol. Cell. Biol. 19:7539-7548(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20094982; PubMed=10629060; Melkar N., Gupta S., Dickens M., Davis R.J.; Interaction of a mitogen-activated protein kinase signaling module with the neuronal protein JTP3."; Mol. Cell. Biol. 20:1030-1043(2000).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20480689; PubMed=11024282;
Ito M., Akechi M., Hirose R., Ichimura M., Takamatsu N., Xu P.,
Nakabeppu Y., Tadayoshi S., Yamamoto K.-I., Yoshioka K.;
"Isoforms of JSAPI scaffold protein generated through alternative
                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1A), FUNCTION, PHOSPHORYLATION, AND INTERACTION WITH MAPK8; MAPK10; MAP2K4 AND MAP3K1.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1A; 1B; 1C; 1D AND 1E), AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21135887; PubMed=11238452;
Verhey K.J., Meyer D., Deehan R., Blenis J., Schnapp B.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6; TISSUE=Brain, and Heart;
                                                                                                                                                                                                                  MEDLINE=99455010; PubMed=10523642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1240-1337 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 255:229-234(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 103:583-594 (2000).
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.";
                                                                                                                                                                                          IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND MAP3K11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIFICITY
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                    BY SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SER
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associated signaling molecules.";
Tassociated signaling molecules.";
Tassociated signaling molecules.";
Tassociated signaling molecules.";
T. Cell Biol. 152:1959-70(2001)

C. FUNCTION: The JUNK-interacting protein (JIP) group of scaffold proteins selectively mediates JUNK signaling by aggregating specific components of the MaPK cascade to form a functional JUNK signaling module. May function as a regulator of vesicle transport, through interations with the JUNK-signaling components and motor proteins.

C. SUBUNIT: Forms homo- or heterooligomeric complexes. The central region of MapkBip1. Binds specific components of the JUNK signaling pathway namelly Mapk8, Mapk9 and Mapk10 to the N-terminal region, Mapk24 and Mapk27 to the central region and map3k11 to the C-terminal region and map3k11 to the C-terminal region and map3k11 to the C-terminal region. Binds the TPR motif-containing C-terminal of kinesin light chain, pre-assembled MapkBip1 scaffolding complexes subcellular location.

C. SUBCELULAR LOCATION: Cytoplasmic; localised in the soma and growth cones of differentiated neurites and the Golgi and vesicles of the early secretory compartment of epithelial cells.

C. HITERNATIVE PRODUCTS:

Name=1c; Synonymm=3h;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoid=09ESN9-6; Sequence=VSP 002776;
TISSUE SPECIFICITY: Highly expressed throughout many regions of the brain and at lower levels in the heart, liver, lung, testes and kidney. All isoforms have been identified in the brain, Mapk61p3A is also expressed in the spleen and lung.
INDUCTION: Expressed in neurites 5 days following initiation of nerve growth factor Ngf induced differentiation. Ngf withdrawal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         results in the down-regulation of MapkBip3 protein by caspase-
                    "Cargo of kinesin identified as JIP scaffolding proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=09ESN9-2; Sequence=VSP_002775, VSP_002777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=3a;
IsoId=Q9ESN9-5; Sequence=VSP_002778, VSP_002779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; GO:0005737; C:cytoplssm; IEP.
GO; GO:0019894; F:Kinesin binding; IPI.
GO; GO:0005078; F:MAP-kinase scaffold activity; IPI.
GO; GO:0019901; F:protein kinase binding; IPI.
GO; GO:0046328; P:regulation of JNK cascade; IDA.
GO; GO:0016192; P:vesicle-mediated transport; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mediated cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9ESN9-4; Sequence=VSP 002775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1c; Synonyms=3b;
IsoId=Q9ESN9-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AB043124; BAB16675.1, -...
EMBL, AB043123; BAB16674.1; -...
EMBL, AB043129; BAB16674.1; -...
EMBL, AB043129; BAB16685.1, -...
EMBL, AB043127; BAB16685.1; -...
EMBL, AB043127; BAB16685.1; JOINED.
EMBL, AB043128; BAB16685.1; JOINED.
EMBL, AF178637; AAF26843.1; -...
EMBL, AF262046; AAG36931.1; -...
EMBL, BC004003; AAH04003.1; -...
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141513 MW; 3FE9D265822D5778 CRC64;

SQ SEQUENCE 1240 AA	Query Match		Qy 220 NSRTYRRONSDN	Db 4 NSKSKRRKN	QY 276 KLPLSQRHVESD	Db 45HTESE	Qy 332PLRYR-	c	88 SMUSASSL	Qy 383VGE	Db 131 DDHSCSCSVCGR	Qy 419 ESVSHT	Db 191 NDLSTKGEVVR	Qy 456 XNKGRNSDF	Db 251 INKTSSEISANF	Qy 488 LLAFLAE	DP 309 LMNSNGQGFLNP	QY 527 SDGYIFDEHDII	Db 367 EDEYADLQRNIX	Qy 575 EKGILPPSPDA	Db 427 FDGELGPSVLA	Qy 610 PLVRLPYMVEHT	Db 487 EAVEKPEHI	Qy 670 EHPDERPHSNDC		Qy 723	Db 574 EGDDEEDTYDS	Qy 769 NSIMAEAEKLL	Db 623 NRLKLL	. 53 23	DT 28-FEB-2003 (Rel. 41 DT 10-OCT-2003 (Rel. 42 DE C-jun-amino-terminal DE protein 3) (JIP-3) (DE activated protein kill DE protein 1) (JSAP1) (JSAP1) (JSAP1)
452 KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPIT 496	:	497 -HPERLGKPNSQIEYTEDEVRIAQL 520	706 MSSQKLGNGISSELIELQKDMKESYRQLVQELRSLYNLQHTHEESQKELMYGVRNDIDAL 765	521 ADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGI 578	766 VKTCTTSLNDADII-LSDYISDQKSKFESKQQDLIANIGKIVSNFLQEQNESLYTK 820	579 LPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVK 625	:   :   :     :		YYVEHPDERP	873 NGSQLLDSKSKAIHSNSRSMYDHCLALAESQKQGVNLEVQTLDRLLQKVKE 923	677 HSNDGWGNASEHVLGKKDHSEDPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEV 736	924 HSEDNTKEKHQQLLDLLESLVGNNDNLIDSIKTPHTELQ 962	TDSSLKANATETLAGLRNNLTLQIMDNNSIMAEAE		781 LLKGSNPSSVSKEKIN 796	 1020 TPSWTRDSSLIKETIN 1035			YNJI YEAST STANDAKD; PKT; 1240 AA. P53935;	01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update)	01-0CT-1996 (Rel. 34, Last annocation update) Hypothetical 141.5 kDa protein in YPT53-RHO2 intergenic region.		<pre>Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.</pre>	NCB1_Tax1D=4932; [1]	SEQUENCE FROM N.A. STRAIN=S288c / FY1679;	MEDLINE=96367601; PubMed=8771715; Garcia-Cantalejo J.M., Boskovic J., Jimenez A.;	"Sequence analysis of a 14.2 KD fragment of Saccharomyces cerevisiae chromosome XIV that includes the ypt53, tRNALeu and gsr m2 genes and	tour new open reading frames."; Yeast 12:599-608(1996).	-!- SIMILARITY: TO S. POMBE SPAC29E6.10C.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; X85811; CAA59826.1; EMBL; Z71367; CAA595967.1; PIR, S52734; S52734. Germonline; 143097; SGD; S0005055; YN1099W

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AATLSSCFSSQSKDTSLDTDSIYEDEDEEDYDDYSEYAEDSEEVSEYEGI 486
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                                                                                                                                       331
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12, Last sequence update)
12, Last sequence update)
13, Last annotation update)
14, Last annotation protein 3 (JNK-interacting (JNK MAP kinase scaffold protein 3) (Mitogen-tinase 8-interacting protein 3) (JNK/SAPK-associated (Sunday driver 2).
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                                                                    NTSRTINWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLL----KQLY
                                    Gaps
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QD8; Q9ESN7; Q9ESN8; Q9ESP0; Q9JLH2; Q9JLH3;
                                    Indels 277;
Length 1240;
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19.8%; Pred. No. 3.4;
ive 85; Mismatches 236;
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